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<110> Ganymed Pharmaceuticals AG
TÜRECI, Özlem
SAHIN, Ugur
HELFTENBEIN, Gerd
SCHLÜTER, Volker

<120> Identification of Tumour-Associated Cell Surface Antigens for Diagnosis and Therapy

<130> VOS-203

<140> US10/573,229
<141> 2006-03-24

<150> PCT/EP2004/010697
<151> 2004-09-23

<150> DE 103 44 799.7
<151> 2003-09-26

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<170> PatentIn Version 3.1

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Ile Gln Val Asp Ala Gln Leu His Thr Pro Val Tyr Phe Phe Leu Ser
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His Leu Ala Phe Leu Asp Ala Cys Cys Ala Ser Val Ile Thr Pro Gln
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Thr Cys Thr Phe Thr Leu Ser Phe Cys Cys Asp Asn Gln Ile Asn Phe
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Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Ser Met
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Gly Ser Gly Lys Ala Val Gly Trp Ser Trp Arg Ser Leu Arg Glu Thr
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Gly Pro Pro Ala Thr Cys Gln Arg Pro Asp Leu Gln Thr Pro Ser Pro
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Pro Lys Glu Ile Cys Ser Ser Gly Leu Arg Pro Leu Thr His Ser Ala
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Leu Thr Lys Gly Leu Pro Asp Ile Thr Val Gly Leu Gln Ile Tyr Asp
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His Leu Leu Gly Val Val Gly Gly Met Thr Phe Leu Glu Ser Glu Pro
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Met Ser Glu Leu Leu Ser Ile Tyr Arg Val Pro Gln Gly Gln Arg Leu
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Thr Lys Asn Phe Glu Val Lys Glu Leu Val Cys Thr Tyr Leu Val Gly
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Gln Leu Pro Tyr Gly Leu Val Ser Tyr Asp Asn Ser Asn Phe Glu Trp
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Tyr Gln Ala Tyr Leu Ala Ala Lys Ala Leu Trp Val Ala Tyr Gln Asn
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Ala Gln Glu Glu Val Phe Phe Ala Lys Asp Gly Glu Val Leu Thr Thr
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Phe Asp Ile Lys Asn Ile Tyr Val Leu Pro Asp Leu Ser Gly Gln Thr
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725 730 735

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755 760 765

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820 825 830

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Cys Ser Cys Val Trp Val Ser Phe Ile Pro Ala His Met His Ala His
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Gly Gly Leu Met Ser Ser Leu Phe Phe Ser Lys Cys Tyr Ile Ile Leu
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35 40 45

Ile Asn Ser Asn Thr Asp Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg
50 55 60

Asp Ile Leu Asn Asn Phe Pro His Ser Ile Ala Arg Gln Lys Arg Ile
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Gln Ser Leu His Tyr Arg Gly Glu Met Gln Gln Tyr Phe Thr Tyr His
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Glu Ser Gly Lys Ser Tyr Tyr Lys Val Lys Asn Leu Gly Val Cys Gly
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Thr Lys Ile Gly Gln Trp Gly Val Asn Thr Gln Val Leu Glu Asp Ile
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ctgtgagcat gcgcgggact tcgcgcaccg ctgcgtgctg cacttctttg ccagcatgcg 960

gagtgagctg caggcgcggg ggctgcgccg gggcaatgca ggcaggagac tcgagctccc 1020

cgcagtgcct gagcccccag aaggcctgga tagtggaagt gggaaggccc acctgcgcgc 1080

aatctccagc cgggagcagg tggaccgcct cctaagcacg tggtactcca gcaagccgcc 1140

gctggacctg gctgcatccc ccgggctctg cgggggtggc cttagccacc gcgcccctac 1200

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ctctgcctag tttctgggtg tggcctccag cgcgcttcac aaactttaat gtggactcgg 1440

ttcaccgagg gccttgttaa atacaggttc agacagtgta gccaggaccg agtctgagat 1500

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<212> PRT
<213> Homo sapiens

<400> 18

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Ser Val Met Asn Gly Ile Cys Leu Leu Leu Ala Ala Val Thr Val Lys
20 25 30

Leu Tyr Ser Ser Phe Asp Phe Asn Cys Pro Cys Leu Val His Tyr Asn
35 40 45

Ala Leu Tyr Gly Leu Gly Leu Leu Leu Thr Pro Pro Leu Ala Leu Phe
50 55 60

Leu Cys Gly Leu Leu Ala Asn Arg Gln Ser Val Val Met Val Glu Glu
65 70 75 80

Trp Arg Arg Pro Ala Gly His Arg Arg Lys Asp Pro Gly Ile Ile Arg
85 90 95

Tyr Met Cys Ser Ser Val Leu Gln Arg Ala Leu Ala Ala Pro Leu Val
100 105 110

Trp Ile Leu Leu Ala Leu Leu Asp Gly Lys Cys Phe Val Cys Ala Phe
115 120 125

Ser Ser Ser Val Asp Pro Glu Lys Phe Leu Asp Phe Ala Asn Met Thr
130 135 140

Pro Ser Gln Val Gln Leu Phe Leu Ala Lys Val Pro Cys Lys Glu Asp
145 150 155 160

Glu Leu Val Arg Asp Ser Pro Ala Arg Lys Ala Val Ser Arg Tyr Leu
165 170 175

Arg Cys Leu Ser Gln Ala Ile Gly Trp Ser Val Thr Leu Leu Leu Ile
180 185 190

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Ile Ala Ala Phe Leu Ala Arg Cys Leu Arg Pro Cys Phe Asp Gln Thr
        195                 200                 205

Val Phe Leu Gln Arg Arg Tyr Trp Ser Asn Tyr Val Asp Leu Glu Gln
    210                 215                 220

Lys Leu Phe Asp Glu Thr Cys Cys Glu His Ala Arg Asp Phe Ala His
225                 230                 235                 240

Arg Cys Val Leu His Phe Phe Ala Ser Met Arg Ser Glu Leu Gln Ala
                245                 250                 255

Arg Gly Leu Arg Arg Gly Asn Ala Gly Arg Arg Leu Glu Leu Pro Ala
            260                 265                 270

Val Pro Glu Pro Pro Glu Gly Leu Asp Ser Gly Ser Gly Lys Ala His
        275                 280                 285

Leu Arg Ala Ile Ser Ser Arg Glu Gln Val Asp Arg Leu Leu Ser Thr
    290                 295                 300

Trp Tyr Ser Ser Lys Pro Pro Leu Asp Leu Ala Ala Ser Pro Gly Leu
305                 310                 315                 320

Cys Gly Gly Gly Leu Ser His Arg Ala Pro Thr Leu Ala Leu Gly Thr
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Arg Leu Ser Gln His Thr Asp Val
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<210> 20
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<223> Oligonucleotide

<400> 20
gaaggcacac acgaagcact 20

<210> 21
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<212> DNA
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ggttccagct ggtgcctggc ctgtgtctct tggatgccct gtggcttcag tccgtctcct 180

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<211> 1151
<212> PRT
<213> Homo sapiens

<400> 22

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Gly Pro Pro Asp Thr Pro Ala Gln Gln Leu Arg Cys Gly Trp Thr Val
20 25 30

Gly Gly Trp Leu Leu Ser Leu Val Arg Gly Leu Leu Pro Cys Leu Pro
35 40 45

Pro Gly Ala Arg Thr Ala Glu Gly Pro Ile Met Val Leu Ala Gly Pro
50 55 60

Leu Ala Val Ser Leu Leu Leu Pro Ser Leu Thr Leu Leu Val Ser His
65 70 75 80

```
Leu Ser Ser Ser Gln Asp Val Ser Ser Glu Pro Ser Ser Glu Gln Gln
                85                  90                  95

Leu Cys Ala Leu Ser Lys His Pro Thr Val Ala Phe Glu Asp Leu Gln
            100                 105                 110

Pro Trp Val Ser Asn Phe Thr Tyr Pro Gly Ala Arg Asp Phe Ser Gln
        115                 120                 125

Leu Ala Leu Asp Pro Ser Gly Asn Gln Leu Ile Val Gly Ala Arg Asn
    130                 135                 140

Tyr Leu Phe Arg Leu Ser Leu Ala Asn Val Ser Leu Leu Gln Ala Thr
145                 150                 155                 160

Glu Trp Ala Ser Ser Glu Asp Thr Arg Arg Ser Cys Gln Ser Lys Gly
                165                 170                 175

Lys Thr Glu Glu Glu Cys Gln Asn Tyr Val Arg Val Leu Ile Val Ala
            180                 185                 190

Gly Arg Lys Val Phe Met Cys Gly Thr Asn Ala Phe Ser Pro Met Cys
        195                 200                 205

Thr Ser Arg Gln Val Gly Asn Leu Ser Arg Thr Ile Glu Lys Ile Asn
    210                 215                 220

Gly Val Ala Arg Cys Pro Tyr Asp Pro Arg His Asn Ser Thr Ala Val
225                 230                 235                 240

Ile Ser Ser Gln Gly Glu Leu Tyr Ala Ala Thr Val Ile Asp Phe Ser
                245                 250                 255

Gly Arg Asp Pro Ala Ile Tyr Arg Ser Leu Gly Ser Gly Pro Pro Leu
            260                 265                 270

Arg Thr Ala Gln Tyr Asn Ser Lys Trp Leu Asn Glu Pro Asn Phe Val
        275                 280                 285

Ala Ala Tyr Asp Ile Gly Leu Phe Ala Tyr Phe Phe Leu Arg Glu Asn
    290                 295                 300

Ala Val Glu His Asp Cys Gly Arg Thr Val Tyr Ser Arg Val Ala Arg
305                 310                 315                 320

Val Cys Lys Asn Asp Val Gly Gly Arg Phe Leu Leu Glu Asp Thr Trp
                325                 330                 335
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Thr Thr Phe Met Lys Ala Arg Leu Asn Cys Ser Arg Pro Gly Glu Val
            340                 345                 350

Pro Phe Tyr Tyr Asn Glu Leu Gln Ser Ala Phe His Leu Pro Glu Gln
        355                 360                 365

Asp Leu Ile Tyr Gly Val Phe Thr Thr Asn Val Asn Ser Ile Ala Ala
    370                 375                 380

Ser Ala Val Cys Ala Phe Asn Leu Ser Ala Ile Ser Gln Ala Phe Asn
385                 390                 395                 400

Gly Pro Phe Arg Tyr Gln Glu Asn Pro Arg Ala Ala Trp Leu Pro Ile
                405                 410                 415

Ala Asn Pro Ile Pro Asn Phe Gln Cys Gly Thr Leu Pro Glu Thr Gly
            420                 425                 430

Pro Asn Glu Asn Leu Thr Glu Arg Ser Leu Gln Asp Ala Gln Arg Leu
        435                 440                 445

Phe Leu Met Ser Glu Ala Val Gln Pro Val Thr Pro Glu Pro Cys Val
    450                 455                 460

Thr Gln Asp Ser Val Arg Phe Ser His Leu Val Val Asp Leu Val Gln
465                 470                 475                 480

Ala Lys Asp Thr Leu Tyr His Val Leu Tyr Ile Gly Thr Glu Ser Gly
                485                 490                 495

Thr Ile Leu Lys Ala Leu Ser Thr Ala Ser Arg Ser Leu His Gly Cys
            500                 505                 510

Tyr Leu Glu Glu Leu His Val Leu Pro Pro Gly Arg Arg Glu Pro Leu
        515                 520                 525

Arg Ser Leu Arg Ile Leu His Ser Ala Arg Ala Leu Phe Val Gly Leu
    530                 535                 540

Arg Asp Gly Val Leu Arg Val Pro Leu Glu Arg Cys Ala Ala Tyr Arg
545                 550                 555                 560

Ser Gln Gly Ala Cys Leu Gly Ala Arg Asp Pro Tyr Cys Gly Trp Asp
                565                 570                 575

Gly Lys Gln Gln Arg Cys Ser Thr Leu Glu Asp Ser Ser Asn Met Ser
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580 585 590

Leu Trp Thr Gln Asn Ile Thr Ala Cys Pro Val Arg Asn Val Thr Arg
595 600 605

Asp Gly Gly Phe Gly Pro Trp Ser Pro Trp Gln Pro Cys Glu His Leu
610 615 620

Asp Gly Asp Asn Ser Gly Ser Cys Leu Cys Arg Ala Arg Ser Cys Asp
625 630 635 640

Ser Pro Arg Pro Arg Cys Gly Gly Leu Asp Cys Leu Gly Pro Ala Ile
645 650 655

His Ile Ala Asn Cys Ser Arg Asn Gly Ala Trp Thr Pro Trp Ser Ser
660 665 670

Trp Ala Leu Cys Ser Thr Ser Cys Gly Ile Gly Phe Gln Val Arg Gln
675 680 685

Arg Ser Cys Ser Asn Pro Ala Pro Arg His Gly Gly Arg Ile Cys Val
690 695 700

Gly Lys Ser Arg Glu Glu Arg Phe Cys Asn Glu Asn Thr Pro Cys Pro
705 710 715 720

Val Pro Ile Phe Trp Ala Ser Trp Gly Ser Trp Ser Lys Cys Ser Ser
725 730 735

Asn Cys Gly Gly Gly Met Gln Ser Arg Arg Arg Ala Cys Glu Asn Gly
740 745 750

Asn Ser Cys Leu Gly Cys Gly Val Glu Phe Lys Thr Cys Asn Pro Glu
755 760 765

Gly Cys Pro Glu Val Arg Arg Asn Thr Pro Trp Thr Pro Trp Leu Pro
770 775 780

Val Asn Val Thr Gln Gly Gly Ala Arg Gln Glu Gln Arg Phe Arg Phe
785 790 795 800

Thr Cys Arg Ala Pro Leu Ala Asp Pro His Gly Leu Gln Phe Gly Arg
805 810 815

Arg Arg Thr Glu Thr Arg Thr Cys Pro Ala Asp Gly Ser Gly Ser Cys
820 825 830

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Asp Thr Asp Ala Leu Val Glu Val Leu Leu Arg Ser Gly Ser Thr Ser
        835                 840                 845

Pro His Thr Val Ser Gly Gly Trp Ala Ala Trp Gly Pro Trp Ser Ser
    850                 855                 860

Cys Ser Arg Asp Cys Glu Leu Gly Phe Arg Val Arg Lys Arg Thr Cys
865                 870                 875                 880

Thr Asn Pro Glu Pro Arg Asn Gly Gly Leu Pro Cys Val Gly Asp Ala
                885                 890                 895

Ala Glu Tyr Gln Asp Cys Asn Pro Gln Ala Cys Pro Val Arg Gly Ala
            900                 905                 910

Trp Ser Cys Trp Thr Ser Trp Ser Pro Cys Ser Ala Ser Cys Gly Gly
        915                 920                 925

Gly His Tyr Gln Arg Thr Arg Ser Cys Thr Ser Pro Ala Pro Ser Pro
    930                 935                 940

Gly Glu Asp Ile Cys Leu Gly Leu His Thr Glu Glu Ala Leu Cys Ala
945                 950                 955                 960

Thr Gln Ala Cys Pro Glu Gly Trp Ser Pro Trp Ser Glu Trp Ser Lys
                965                 970                 975

Cys Thr Asp Asp Gly Ala Gln Ser Arg Ser Arg His Cys Glu Glu Leu
            980                 985                 990

Leu Pro Gly Ser Ser Ala Cys Ala  Gly Asn Ser Ser Gln  Ser Arg Pro
        995                 1000                1005

Cys Pro  Tyr Ser Glu Ile Pro  Val Ile Leu Pro Ala  Ser Ser Met
    1010                1015                1020

Glu Glu  Ala Thr Asp Cys Ala  Gly Phe Asn Leu Ile  His Leu Val
    1025                1030                1035

Ala Thr  Gly Ile Ser Cys Phe  Leu Gly Ser Gly Leu  Leu Thr Leu
    1040                1045                1050

Ala Val  Tyr Leu Ser Cys Gln  His Cys Gln Arg Gln  Ser Gln Glu
    1055                1060                1065

Ser Thr  Leu Val His Pro Ala  Thr Pro Asn His Leu  His Tyr Lys
    1070                1075                1080
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Gly Gly Gly Thr Pro Lys Asn Glu Lys Tyr Thr Pro Met Glu Phe
1085 1090 1095

Lys Thr Leu Asn Lys Asn Asn Leu Ile Pro Asp Asp Arg Ala Asn
1100 1105 1110

Phe Tyr Pro Leu Gln Gln Thr Asn Val Tyr Thr Thr Thr Tyr Tyr
1115 1120 1125

Pro Ser Pro Leu Asn Lys His Ser Phe Arg Pro Glu Ala Ser Pro
1130 1135 1140

Gly Gln Arg Cys Phe Pro Asn Ser
1145 1150

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<211> 21
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<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 23
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<210> 24
<211> 21
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<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 24
gttgcacgtc ttgaactcca c 21

<210> 25
<211> 1299
<212> DNA
<213> Homo sapiens

<400> 25
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gggactcctg agtggggtca acaagtactc cacagccttt gggcgcatct ggctgtctct 180

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ccacaaggac ttcgactgca atactcgcca gcccggctgc tccaacgtct gctttgatga 300

gttcttccct gtgtcccatg tgcgcctctg ggccctgcag cttatcctgg tgacatgccc 360

ctcactgctc gtggtcatgc acgtggccta ccgggaggtt caggagaaga ggcaccgaga 420

agcccatggg gagaacagtg ggcgcctcta cctgaacccc ggcaagaagc ggggtgggct 480

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<210> 26
<211> 273
<212> PRT
<213> Homo sapiens

<400> 26

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
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Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
20 25 30

Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His
35 40 45

Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys
50 55 60

Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
65 70 75 80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
85 90 95

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Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn
            100                 105                 110

Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp
        115                 120                 125

Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala
    130                 135                 140

Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro
145                 150                 155                 160

Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe
                165                 170                 175

Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala
            180                 185                 190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu
        195                 200                 205

Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala
    210                 215                 220

Met Cys Thr Gly His His Pro His Gly Thr Thr Ser Ser Cys Lys Gln
225                 230                 235                 240

Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser His
                245                 250                 255

Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile
            260                 265                 270

Leu
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<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 27
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<210> 28

<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 28
gaactcatca aagcagacg 19

<210> 29
<211> 1528
<212> DNA
<213> Homo sapiens

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tctgtgcgtc ctgcacccac atctttctct gtcccctcct tgccctgtct ggaggctgct 180

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gtccttgtgg ttcctctcta cctggggaaa taaggtgcag cggccatggc tacagcaaga 300

ccccccctgga tgtgggtgct ctgtgctctg atcacagcct tgcttctggg ggtcacagag 360

catgttctcg ccaacaatga tgtttcctgt gaccaccccct ctaacaccgt gccctctggg 420

agcaaccagg acctgggagc tggggccggg gaagacgccc ggtcggatga cagcagcagc 480

cgcatcatca atggatccga ctgcgatatg cacacccagc cgtggcaggc cgcgctgttg 540

ctaaggccca accagctcta ctgcggggcg gtgttggtgc atccacagtg gctgctcacg 600

gccgcccact gcaggaagaa agttttcaga gtccgtctcg gccactactc cctgtcacca 660

gtttatgaat ctgggcagca gatgttccag ggggtcaaat ccatccccca ccctggctac 720

tcccaccctg gccactctaa cgacctcatg ctcatcaaac tgaacagaag aattcgtccc 780

actaaagatg tcagacccat caacgtctcc tctcattgtc cctctgctgg gacaaagtgc 840

ttggtgtctg gctgggggac aaccaagagc ccccaagtgc acttccctaa ggtcctccag 900

tgcttgaata tcagcgtgct aagtcagaaa aggtgcgagg atgcttaccc gagacagata 960

gatgacacca tgttctgcgc cggtgacaaa gcaggtagag actcctgcca gggtgattct 1020

gggggggcctg tggtctgcaa tggctccctg cagggactcg tgtcctgggg agattaccct 1080

tgtgcccggc ccaacagacc gggtgtctac acgaacctct gcaagttcac caagtggatc 1140

caggaaacca tccaggccaa ctcctgagtc atcccaggac tcagcacacc ggcatcccca 1200

cctgctgcag ggacagccct gacactcctt tcagaccctc attccttccc agagatgttg 1260

agaatgttca tctctccagc ccctgacccc atgtctcctg gactcagggt ctgcttcccc 1320

cacattgggc tgaccgtgtc tctctagttg aaccctggga acaatttcca aaactgtcca 1380

gggcgggggt tgcgtctcaa tctccctggg gcactttcat cctcaagctc agggcccatc 1440

ccttctctgc agctctgacc caaatttagt cccagaaata aactgagaag tggaaaaaaa 1500

aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1528

<210> 30
<211> 293
<212> PRT
<213> Homo sapiens

<400> 30

Met Ala Thr Ala Arg Pro Pro Trp Met Trp Val Leu Cys Ala Leu Ile
1 5 10 15

Thr Ala Leu Leu Leu Gly Val Thr Glu His Val Leu Ala Asn Asn Asp
20 25 30

Val Ser Cys Asp His Pro Ser Asn Thr Val Pro Ser Gly Ser Asn Gln
35 40 45

Asp Leu Gly Ala Gly Ala Gly Glu Asp Ala Arg Ser Asp Asp Ser Ser
50 55 60

Ser Arg Ile Ile Asn Gly Ser Asp Cys Asp Met His Thr Gln Pro Trp
65 70 75 80

Gln Ala Ala Leu Leu Leu Arg Pro Asn Gln Leu Tyr Cys Gly Ala Val
85 90 95

Leu Val His Pro Gln Trp Leu Leu Thr Ala Ala His Cys Arg Lys Lys
100 105 110

Val Phe Arg Val Arg Leu Gly His Tyr Ser Leu Ser Pro Val Tyr Glu
115 120 125

Ser Gly Gln Gln Met Phe Gln Gly Val Lys Ser Ile Pro His Pro Gly
130 135 140

Tyr Ser His Pro Gly His Ser Asn Asp Leu Met Leu Ile Lys Leu Asn
145 150 155 160

Arg Arg Ile Arg Pro Thr Lys Asp Val Arg Pro Ile Asn Val Ser Ser
165 170 175

His Cys Pro Ser Ala Gly Thr Lys Cys Leu Val Ser Gly Trp Gly Thr
180 185 190

```
Thr Lys Ser Pro Gln Val His Phe Pro Lys Val Leu Gln Cys Leu Asn
        195                 200                 205

Ile Ser Val Leu Ser Gln Lys Arg Cys Glu Asp Ala Tyr Pro Arg Gln
    210                 215                 220

Ile Asp Asp Thr Met Phe Cys Ala Gly Asp Lys Ala Gly Arg Asp Ser
225                 230                 235                 240

Cys Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly Ser Leu Gln
                245                 250                 255

Gly Leu Val Ser Trp Gly Asp Tyr Pro Cys Ala Arg Pro Asn Arg Pro
            260                 265                 270

Gly Val Tyr Thr Asn Leu Cys Lys Phe Thr Lys Trp Ile Gln Glu Thr
        275                 280                 285

Ile Gln Ala Asn Ser
    290
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<210> 31
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 31
cagaaaaggt gcgaggatg 19

<210> 32
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 32
ctgggatgac tcaggagttg g 21

<210> 33
<211> 636
<212> DNA
<213> Homo sapiens

<400> 33
atgacagaag cagcatcgct tgtccctaag aggccaagga ggctcagagg cagccacaag 60

ctgcgagttc tggcatggcc agtggtcgtg gtggtgaact ttgtttggca gtgcaacggc 120

agcattgctc acaccttcct ggagctaagc ttcgcctgcc ctggaggaag gtacgcaggc 180

agtcgcccag ccccggttgc agggatggac cgcgaccagc agagggcaga aagtgcctgt 240

gtcccccatt ctcgatcccg gggccccaac ctcccatcgg ctcagtcccc cgcccaatct 300

ctgccaggcc cggagctttc ccagacccct cacccacact ccaggctcac tccccgttcc 360

tgggcctggg ccccccttgc acgagtccag ggccagccgt cctcgccttc tgcccgcccc 420

cgtccttcgt tcctgggagc cggccctctc cgcggaccaa gcggccccga gcaggcgccg 480

ccgcccgggg gactccgact cagcccccgc gacctacctc ggccgacagt cgggggttcc 540

caagcggcca ctcccggccg gcgccgtccc ctggcggagc cgccgcgctc cctgccgtcc 600

gcgcagtctg gcctcgctcg gggccactcc tcgtag 636

<210> 34
<211> 211
<212> PRT
<213> Homo sapiens

<400> 34

Met Thr Glu Ala Ala Ser Leu Val Pro Lys Arg Pro Arg Arg Leu Arg
1 5 10 15

Gly Ser His Lys Leu Arg Val Leu Ala Trp Pro Val Val Val Val Val
20 25 30

Asn Phe Val Trp Gln Cys Asn Gly Ser Ile Ala His Thr Phe Leu Glu
35 40 45

Leu Ser Phe Ala Cys Pro Gly Gly Arg Tyr Ala Gly Ser Arg Pro Ala
50 55 60

Pro Val Ala Gly Met Asp Arg Asp Gln Gln Arg Ala Glu Ser Ala Cys
65 70 75 80

Val Pro His Ser Arg Ser Arg Gly Pro Asn Leu Pro Ser Ala Gln Ser
85 90 95

Pro Ala Gln Ser Leu Pro Gly Pro Glu Leu Ser Gln Thr Pro His Pro
100 105 110

His Ser Arg Leu Thr Pro Arg Ser Trp Ala Trp Ala Pro Leu Ala Arg
115 120 125

Val Gln Gly Gln Pro Ser Ser Pro Ser Ala Arg Pro Arg Pro Ser Phe
130 135 140

```
Leu Gly Ala Gly Pro Leu Arg Gly Pro Ser Gly Pro Glu Gln Ala Pro
145                 150                 155                 160

Pro Pro Gly Gly Leu Arg Leu Ser Pro Arg Asp Leu Pro Arg Pro Thr
                165                 170                 175

Val Gly Gly Ser Gln Ala Ala Thr Pro Gly Arg Arg Arg Pro Leu Ala
            180                 185                 190

Glu Pro Pro Arg Ser Leu Pro Ser Ala Gln Ser Gly Leu Ala Arg Gly
        195                 200                 205

His Ser Ser
    210
```

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 35
tgctctcact gtggtcctca g 21

<210> 36
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 36
tttgtaaagc tccagcgcta c 21

<210> 37
<211> 969
<212> DNA
<213> Homo sapiens

<400> 37
atgaaggact gtaggaacaa tggcaaggat tgtcaaagtg cccctgcaac acgtaggcac 60

ctcttctctg aagctgccct gccccttat cgtctttccc aagggcactt cctcacagcc 120

ctgggggcc tcatggcggt gccattcatc ctggccaagg acctgtgcct gcagcaggac 180

cccctgacac agagctacct catcagcacc attttctttg ctccagcatc tgcatgctcc 240

tgcaagctgc ccattcccca gggaggtacg tttgcttttg tggtaatttc tctggccatg 300

ctctcccttc cctcctggaa ttgccctgag tggacactca gtgccagcca ggtgaacacc 360

aactttccag aattcactca gaaatggcag aagaggatcc aagagggtgc tatcatggtc 420

acttcctgtg tccggatgct ggtgggcttc tcaggcctga ctggctttct catgggtttc 480

atctgctcct tggccgttgc tccaactaac tgcctagtgg ccctgcccct cttggattct 540

gcaggcaata atgccgggat ccagtggggg atttctgcca tgtattgctt cgtgttgcgt 600

cttcgcaagg atgagctctg gccatttggt tctccacggc tgcgtttgcc accatcccca 660

ccccgtgatc ggaggcatgt ccccaccccc gtgatcggag gcatgaccct gtttggggtc 720

atcactgccg tggggatctc caatctgcag tacgtggaca tgaacttgtc caggagcctc 780

ttcgcctttg gcttctccat ctactgtggg ctcaccattc ccaaccgggt gagcaaaaac 840

cccgagatgc tccagacagg gattctccag ccggaccagg ttgttcagat gctgctgacc 900

atgggcatgt tcatcagtgg atttctgggt tttcttctag acaacaccat ccccgagctc 960

cttcaataa 969

<210> 38
<211> 322
<212> PRT
<213> Homo sapiens

<400> 38

Met Lys Asp Cys Arg Asn Asn Gly Lys Asp Cys Gln Ser Ala Pro Ala
1 5 10 15

Thr Arg Arg His Leu Phe Ser Glu Ala Ala Leu Pro Pro Tyr Arg Leu
20 25 30

Ser Gln Gly His Phe Leu Thr Ala Leu Gly Gly Leu Met Ala Val Pro
35 40 45

Phe Ile Leu Ala Lys Asp Leu Cys Leu Gln Gln Asp Pro Leu Thr Gln
50 55 60

Ser Tyr Leu Ile Ser Thr Ile Phe Phe Ala Pro Ala Ser Ala Cys Ser
65 70 75 80

Cys Lys Leu Pro Ile Pro Gln Gly Gly Thr Phe Ala Phe Val Val Ile
85 90 95

Ser Leu Ala Met Leu Ser Leu Pro Ser Trp Asn Cys Pro Glu Trp Thr
100 105 110

Leu Ser Ala Ser Gln Val Asn Thr Asn Phe Pro Glu Phe Thr Gln Lys
115 120 125

```
Trp Gln Lys Arg Ile Gln Glu Gly Ala Ile Met Val Thr Ser Cys Val
    130                 135                 140

Arg Met Leu Val Gly Phe Ser Gly Leu Thr Gly Phe Leu Met Gly Phe
145                 150                 155                 160

Ile Cys Ser Leu Ala Val Ala Pro Thr Asn Cys Leu Val Ala Leu Pro
                165                 170                 175

Leu Leu Asp Ser Ala Gly Asn Asn Ala Gly Ile Gln Trp Gly Ile Ser
            180                 185                 190

Ala Met Tyr Cys Phe Val Leu Arg Leu Arg Lys Asp Glu Leu Trp Pro
        195                 200                 205

Phe Gly Ser Pro Arg Leu Arg Leu Pro Pro Ser Pro Pro Arg Asp Arg
    210                 215                 220

Arg His Val Pro Thr Pro Val Ile Gly Gly Met Thr Leu Phe Gly Val
225                 230                 235                 240

Ile Thr Ala Val Gly Ile Ser Asn Leu Gln Tyr Val Asp Met Asn Leu
                245                 250                 255

Ser Arg Ser Leu Phe Ala Phe Gly Phe Ser Ile Tyr Cys Gly Leu Thr
            260                 265                 270

Ile Pro Asn Arg Val Ser Lys Asn Pro Glu Met Leu Gln Thr Gly Ile
        275                 280                 285

Leu Gln Pro Asp Gln Val Val Gln Met Leu Leu Thr Met Gly Met Phe
    290                 295                 300

Ile Ser Gly Phe Leu Gly Phe Leu Leu Asp Asn Thr Ile Pro Glu Leu
305                 310                 315                 320

Leu Gln
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<210> 39
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 39
atggcggtgc cattcatcct 20

<210> 40
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 40
caggagggaa gggagagcat 20

<210> 41
<211> 1679
<212> DNA
<213> Homo sapiens

<400> 41
gaggaggcgc gcgtcgccgc cccgcgtccc gcctgcggcc cgcgcccccg gcgtcaccgc 60

ctcctgcccg cctgcccgcc tgcccgcctg cccgcctacc cgcctacccg cctacccgcc 120

tacccccctg ccggcctgcc gtccttccac gcggagagcc atggagggag tgagcgcgct 180

gctggcccgc tgccccacgg ccggcctggc cggcggcctg ggggtcacgg cgtgcgccgc 240

ggccggcgtg ttgctctacc ggatcgcgcg gaggatgaag ccaacgcaca cgatggtcaa 300

ctgctggttc tgcaaccagg atacgctggt gccctatggg aaccgcaact gctgggactg 360

tccccactgc gagcagtaca acggcttcca ggagaacggc gactacaaca agccgatccc 420

cgcccagtac ttggagcacc tgaaccacgt ggtgagcagc gcgcccagcc tgcgcgaccc 480

ttcgcagccg cagcagtggg tgagcagcca agtcctgctg tgcaagaggt gcaaccacca 540

ccagaccacc aagatcaagc agctggccgc cttcgctccc cgcgaggagg gcaggtatga 600

cgaggaggtc gaggtgtacc ggcatcacct ggagcagatg tacaagctgt gccggccgtg 660

ccaagcggct gtggagtact acatcaagca ccagaaccgc cagctgcgcg ccctgttgct 720

cagccaccag ttcaagcgcc gggaggccga ccagacccac gcacagaact tctcctccgc 780

cgtgaagtcc ccggtccagg tcatcctgct ccgtgccctc gccttcctgg cctgcgcctt 840

cctactgacc accgcgctgt atggggccag cggacacttc gccccaggca ccactgtgcc 900

cctggccctg ccacctggtg gcaatggctc agccacacct gacaatggca ccacccctgg 960

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cacctgcctg tgggccctgc tgctggggct gcacctggct gagcagcacc tgcaggccgc 1200

ctcgcctagc tggctagaca cgctcaagtt cagcaccaca tctttgtgct gcctggttgg 1260

cttcacggcg gctgtggcca caaggaaggc aacgggccca cggaggttcc ggccccgaag 1320

gtcagagaag cagccatgac tgcgggggga ggacacacgg atgctcaggc ccaggctttg 1380

ccaggtccga agcgggcccc tctctgtcct gcctcttttc acctgctcac gccctcccac 1440

ccccacccta cagccccagg tcctggccca gtccctccac tgcctcgaag agtcagtctg 1500

ccctgccttt tcctttcggg caccaccagc catccccgag tgccctgtag ccactcacca 1560

ctgctgccac ctctctggcc aatggccctt tcactggcct ggtgactgga atgtgggcag 1620

cgcccacaca ggctctggcc catggcttcc tactggcagc tccaggcacc cccctctca 1679

<210> 42
<211> 392
<212> PRT
<213> Homo sapiens

<400> 42

Met Glu Gly Val Ser Ala Leu Leu Ala Arg Cys Pro Thr Ala Gly Leu
1 5 10 15

Ala Gly Gly Leu Gly Val Thr Ala Cys Ala Ala Ala Gly Val Leu Leu
20 25 30

Tyr Arg Ile Ala Arg Arg Met Lys Pro Thr His Thr Met Val Asn Cys
35 40 45

Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn Arg Asn Cys
50 55 60

Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln Glu Asn Gly
65 70 75 80

Asp Tyr Asn Lys Pro Ile Pro Ala Gln Tyr Leu Glu His Leu Asn His
85 90 95

Val Val Ser Ser Ala Pro Ser Leu Arg Asp Pro Ser Gln Pro Gln Gln
100 105 110

Trp Val Ser Ser Gln Val Leu Leu Cys Lys Arg Cys Asn His His Gln
115 120 125

Thr Thr Lys Ile Lys Gln Leu Ala Ala Phe Ala Pro Arg Glu Glu Gly
130 135 140

Arg Tyr Asp Glu Glu Val Glu Val Tyr Arg His His Leu Glu Gln Met
145 150 155 160

Tyr Lys Leu Cys Arg Pro Cys Gln Ala Ala Val Glu Tyr Tyr Ile Lys
165 170 175

```
His Gln Asn Arg Gln Leu Arg Ala Leu Leu Leu Ser His Gln Phe Lys
            180                 185                 190

Arg Arg Glu Ala Asp Gln Thr His Ala Gln Asn Phe Ser Ser Ala Val
        195                 200                 205

Lys Ser Pro Val Gln Val Ile Leu Leu Arg Ala Leu Ala Phe Leu Ala
    210                 215                 220

Cys Ala Phe Leu Leu Thr Thr Ala Leu Tyr Gly Ala Ser Gly His Phe
225                 230                 235                 240

Ala Pro Gly Thr Thr Val Pro Leu Ala Leu Pro Pro Gly Gly Asn Gly
                245                 250                 255

Ser Ala Thr Pro Asp Asn Gly Thr Thr Pro Gly Ala Glu Gly Trp Arg
            260                 265                 270

Gln Leu Leu Gly Leu Leu Pro Glu His Met Ala Glu Lys Leu Cys Glu
        275                 280                 285

Ala Trp Ala Phe Gly Gln Ser His Gln Thr Gly Val Val Ala Leu Gly
    290                 295                 300

Leu Leu Thr Cys Leu Leu Ala Met Leu Leu Ala Gly Arg Ile Arg Leu
305                 310                 315                 320

Arg Arg Ile Asp Ala Phe Cys Thr Cys Leu Trp Ala Leu Leu Leu Gly
                325                 330                 335

Leu His Leu Ala Glu Gln His Leu Gln Ala Ala Ser Pro Ser Trp Leu
            340                 345                 350

Asp Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu Val Gly Phe
        355                 360                 365

Thr Ala Ala Val Ala Thr Arg Lys Ala Thr Gly Pro Arg Arg Phe Arg
    370                 375                 380

Pro Arg Arg Ser Glu Lys Gln Pro
385                 390
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<210> 43
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 43
ctacatcaag caccagaacc gcc 23

<210> 44
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 44
ggacttcacg gcggaggag 19

<210> 45
<211> 727
<212> DNA
<213> Homo sapiens

<400> 45
aggcagttgc gggttgcagg agttcaggaa aggaggtggg actagagtca acctggaata 60

gctctacagt aacaatggca gccttttttgt tgctgggaca tccatacagg caacttagct 120

ggtgaaagga ctctggattg gttggcagtc tgcttttttt tttccaaggt gatcacttta 180

ctgtagaaga aatgaggtta acagaaaaga gtgagggaga acaacaactc aagcccaaca 240

actctaatgc acccaatgaa gatcaagaag aagaaatcca acagtcagaa cagcatactc 300

cagcaaggca gcgaacacaa agagcagaca cacagccatc cagatgtcga ttgccttcac 360

gtaggacacc tacaacatcc agcgacagaa cgatcaacct tcttgaagtc cttccgtggc 420

ctactgagtg gattttcaac ccctatcgat tgcctgctct ttttgagctt tatcctgaat 480

ttcttctggt gtttaaagaa gccttccatg acatatccca ttgtctgaaa gcccagatgg 540

aaaagatcgg actgcccatc atactccacc tcttcgcact ctccaccctc tacttctaca 600

agtttttcct tcctacaatt ctttcccttt ctttctttat tcttcttgta cttctgcttc 660

tgctttttat tattgtcttc attctgatct tcttctgatt cttttgtttc aataaacagc 720

aatgagc 727

<210> 46
<211> 168
<212> PRT
<213> Homo sapiens

<400> 46

Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys Pro Asn
1 5 10 15

```
Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Glu Ile Gln Gln Ser
            20                  25                  30

Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp Thr Gln
        35                  40                  45

Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr Ser Ser
    50                  55                  60

Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr Glu Trp
65                  70                  75                  80

Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr Pro Glu
                85                  90                  95

Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His Cys Leu
            100                 105                 110

Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His Leu Phe
        115                 120                 125

Ala Leu Ser Thr Leu Tyr Phe Tyr Lys Phe Phe Leu Pro Thr Ile Leu
    130                 135                 140

Ser Leu Ser Phe Phe Ile Leu Leu Val Leu Leu Leu Leu Leu Phe Ile
145                 150                 155                 160

Ile Val Phe Ile Leu Ile Phe Phe
                165
```

<210> 47
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 47
gctggtgaaa ggactctgga 20

<210> 48
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 48
tcgctggatg ttgtaggtgt 20

<210> 49
<211> 950
<212> DNA
<213> Homo sapiens

<400> 49
gcgagcccga gcaggcagac gcgcggccgg cggtctgggg gcgcgccgcc tcccggtccc 60

caaaatgtga agcggggagg gcggagacgc agagacggcc cggccgggcg ccctcgccgc 120

cctccggcag ccgcgccgct ccctccgctg cacgcccagg cctgagcagc gaggccaccg 180

ggccgcgcgc tcccagcttc gctcggacgc ggcttcggcc cgcagagggt tcgtggcccg 240

gacgcggcga gagctgggcc caggacggtg cgtccggcct cgcccgcggc tgctcgcacc 300

aacaagtttg aacaatgatc accgtcaacc ccgatgggaa gataatggtc agaagatgcc 360

tggtcaccct gagacccttt cggctttttg tcctgggcat cggcttcttc actctctgct 420

tcctgatgac gtctctggga ggccagttct cggcccggcg cctgggggac tcgccattca 480

ccatccgcac agaagtgatg gggggccccg agtcccgcgg cgtcctgcgc aagatgagcg 540

acctgctgga gctgatggtg aagcgcatgg acgcactggc caggctggag aacagcagtg 600

agctgcaccg ggccggcggc gacctgcact ttcccgcaga caggatgccc cctggggccg 660

gcctcatgga gcggatccag gctattgccc agaacgtctc cgacatcgct gtgaaggtgg 720

accagatcct gcgccacagt ctgctcctgc acagcaaggt gtcagaaggc cggcgggacc 780

agtgtgaggc acccagtgac cccaagttcc ctgactgctc agggaaggtg gcagtggatg 840

cgtgcccgct ggacctctga cccctgctac gccttctttg gggtggacgg caccgagtgc 900

tccttcctca tctacctcag tgaggtcgag tggttctgcc ccccgctgcc 950

<210> 50
<211> 181
<212> PRT
<213> Homo sapiens

<400> 50

Met Ile Thr Val Asn Pro Asp Gly Lys Ile Met Val Arg Arg Cys Leu
1 5 10 15

Val Thr Leu Arg Pro Phe Arg Leu Phe Val Leu Gly Ile Gly Phe Phe
20 25 30

Thr Leu Cys Phe Leu Met Thr Ser Leu Gly Gly Gln Phe Ser Ala Arg
35 40 45

Arg Leu Gly Asp Ser Pro Phe Thr Ile Arg Thr Glu Val Met Gly Gly
50 55 60

Pro Glu Ser Arg Gly Val Leu Arg Lys Met Ser Asp Leu Leu Glu Leu
65 70 75 80

Met Val Lys Arg Met Asp Ala Leu Ala Arg Leu Glu Asn Ser Ser Glu
85 90 95

Leu His Arg Ala Gly Gly Asp Leu His Phe Pro Ala Asp Arg Met Pro
100 105 110

Pro Gly Ala Gly Leu Met Glu Arg Ile Gln Ala Ile Ala Gln Asn Val
115 120 125

Ser Asp Ile Ala Val Lys Val Asp Gln Ile Leu Arg His Ser Leu Leu
130 135 140

Leu His Ser Lys Val Ser Glu Gly Arg Arg Asp Gln Cys Glu Ala Pro
145 150 155 160

Ser Asp Pro Lys Phe Pro Asp Cys Ser Gly Lys Val Ala Val Asp Ala
165 170 175

Cys Pro Leu Asp Leu
180

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 51
agatgcctgg tcaccctgag a 21

<210> 52
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 52
ggccccccat cacttctgtg 20

<210> 53
<211> 396
<212> DNA
<213> Homo sapiens

<400> 53

ctgcaagacc gcatcgccac gttcttcttc ccaaaaggca tgatgctcac cacggctgcg 60

ctgatgctct tcttcttaca cctgggcatc ttcatcagag acgtgcacaa cttctgcatc 120

acctaccact atgaccacat gagctttcac tacacggtcg tcctgatgtt ctcccaggtg 180

atcagcatct gctgggctgc catggggtca ctctatgctg agatgacaga aaacaatgct 240

caacggagcc atgttcttca accgcctgtc cttggagttt ctggccatcg agtaccggga 300

ggagcaccac tgaggcctgg ggagtcggaa cagggctaag gaggggaag caaaaggctg 360

cctcgggtgt tttaataaag ttgttgttta tttcca 396

<210> 54
<211> 99
<212> PRT
<213> Homo sapiens

<400> 54

Met Met Leu Thr Thr Ala Ala Leu Met Leu Phe Phe Leu His Leu Gly
1 5 10 15

Ile Phe Ile Arg Asp Val His Asn Phe Cys Ile Thr Tyr His Tyr Asp
20 25 30

His Met Ser Phe His Tyr Thr Val Val Leu Met Phe Ser Gln Val Ile
35 40 45

Ser Ile Cys Trp Ala Ala Met Gly Ser Leu Tyr Ala Glu Met Thr Glu
50 55 60

Asn Asn Ala Gln Arg Ser His Val Leu Gln Pro Pro Val Leu Gly Val
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Ser Gly His Arg Val Pro Gly Gly Ala Pro Leu Arg Pro Gly Glu Ser
85 90 95

Glu Gln Gly

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<400> 56
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atatacaggg gaggctggag taggcatgca ggttaccacc catacctcgg ctgtatagtg 240

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agaaggcaaa tgtttaactg gactcattgg agtatgggaa cagctgctag aataatagca 360

gacttaaaac aatctggaaa atgtgggtgc atctctttta aggattggta gattacgcag 420

ccataaaaaa gaatgaagtc atgtcttttg tagcaacatg gatgctgctg gaagtgatta 480

tcctacatga attaatgcag aaacagaaaa tcacatacca catgttctca cttataaat 539

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<211> 133
<212> PRT
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<400> 58

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20 25 30

Ala Trp Phe Gln Val His Arg Met Leu Met Phe Thr Thr Thr Val Leu
35 40 45

Thr Cys Ile Ala Phe Val Met Pro Phe Ile Tyr Arg Gly Gly Trp Ser
50 55 60

Arg His Ala Gly Tyr His Pro Tyr Leu Gly Cys Ile Val Met Thr Leu
65 70 75 80

Ala Val Leu Gln Pro Leu Leu Ala Val Phe Arg Pro Pro Leu His Asp
85 90 95

Pro Arg Arg Gln Met Phe Asn Trp Thr His Trp Ser Met Gly Thr Ala
100 105 110

Ala Arg Ile Ile Ala Asp Leu Lys Gln Ser Gly Lys Cys Gly Cys Ile
115 120 125

Ser Phe Lys Asp Trp
130

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<211> 129
<212> PRT
<213> Homo sapiens

<400> 62

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20 25 30

Leu Leu Thr Trp Ser Leu Phe Thr Ala Trp Leu Arg Pro Pro Thr Leu
35 40 45

Leu Gln Gly Pro Arg Thr Ser Pro Gln Gly Ser Pro Pro Arg Ser Pro
50 55 60

Trp Gly Asp Cys Ala Glu Pro Ser Cys Leu Cys Glu Met Lys Ile Arg
65 70 75 80

Arg Arg Arg His Glu Gly Pro Ala Trp Gly Gln Ser Gly Phe Leu Ala
85 90 95

Gly Gly Leu His Leu Val Pro Ser Ser Leu Ser Leu Ala Ala Cys Gly
100 105 110

Val Val Arg Met Lys Gly Leu Trp Gly Arg Gly Ala Gly Ile Arg Gly
115 120 125

Arg

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<212> PRT
<213> Homo sapiens

<400> 66

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Gly Pro Arg Arg Gln Tyr Thr Thr Gln Arg Asn Ile Leu Ser Thr Phe
20 25 30

Ser Leu Phe His Phe Ile Val Phe Ser Pro Ser Phe Leu Ser Phe Ser
35 40 45

Leu Leu Leu Ser Phe Ser Ser Leu Leu Phe Pro Leu Val Phe Asn Phe
50 55 60

Asn Phe Asn Phe Trp Pro Ser Tyr Thr Ser Ile Cys Leu Ser Arg Lys
65 70 75 80

Leu Asn Ser Arg Gln Leu Ile Ile His Leu Ile Ser Ser Ala Lys Gln
85 90 95

Met Pro Ser Met Val Ser Phe Val Ile Arg Leu Leu Trp Asp Gln Asn
100 105 110

Val Ser Tyr Ser Ser Gly Lys Asn Glu Thr
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<400> 70

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Arg Ala Thr Gly Ile Thr Gly Asn Phe Ala Asn Ile Gly Gly Ala Leu
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Ala Ser Leu Met Met Ile Leu Ser Ile Tyr Ser Arg Pro Leu Pro Trp
35 40 45

Ile Ile Tyr Gly Val Phe Ala Ile Leu Ser Gly Leu Val Val Leu Leu
50 55 60

Leu Pro Glu Thr Arg Asn Gln Pro Leu Leu Asp Ser Ile Gln Asp Val
65 70 75 80

Glu Asn Glu Gly Val Asn Ser Leu Ala Ala Pro Gln Arg Ser Ser Val
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Leu

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<400> 72
agtgattccc agtagctctt c 21

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Ile Ile Ile Ile Ile Ile Ile Phe Arg Trp Ser Leu Ala Leu Ser Leu
35 40 45

Arg Leu Glu Cys Ser Gly Ala Ile Ser Ala Arg Cys Lys Leu Arg Leu
50 55 60

Val Gly Ser Cys His Ser Arg Ala Ser Ala Ser Gln Val Ala Gly Thr
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Pro Glu Ser Glu Ser Val Leu Val Leu Thr Val Leu Met Pro Thr Glu
35 40 45

Glu Ala Tyr Ala Leu Pro Leu Val Val Lys Val Val Asp Asn Trp Ala
50 55 60

Phe Gly Gln Gln Thr Val Thr Gly Gln Ala Asn Ile Asp Phe Leu Gln
65 70 75 80

Pro Tyr Phe Cys Asp Pro Trp Ala Gln Asp Tyr Met His Pro Lys Leu
85 90 95

Pro Thr Leu Ser Glu Lys Lys His Gln Asp Phe Leu Gly Tyr Leu Tyr
100 105 110

Arg Lys Phe Trp Phe Lys Ser Ser Lys Ala Glu Asp Glu Tyr Glu His
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Glu Val Asp Trp Trp Ser Lys Leu Phe Trp Ala Thr Asp Glu His Lys
130 135 140

Ser Leu Lys Tyr Lys Tyr Lys Asp Tyr His Thr Leu Lys Val Tyr Glu
145 150 155 160

Cys Glu Leu Glu Ala Val Pro Ala Phe Gln Gly Leu Gln Asp Phe Cys
165 170 175

Gln Thr Phe Lys Leu Tyr Gln Glu Gln Pro Lys Leu Asp Ser Pro Val
180 185 190

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Val Gly Glu Phe Lys Gly Leu Phe Arg Ile Tyr Pro Phe Pro Glu Asn
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Pro Glu Ala Pro Lys Pro Pro Leu Gln Phe Leu Val Trp Pro Glu Arg
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Glu Asp Phe Pro Gln Pro Cys Leu Val Arg Val Tyr Met Val Arg Ala
225                 230                 235                 240

Ile Asn Leu Gln Pro Gln Asp Tyr Asn Gly Leu Cys Asp Pro Tyr Val
                245                 250                 255

Ile Leu Lys Leu Gly Lys Thr Glu Leu Gly Asn Arg Asp Met Tyr Gln
            260                 265                 270

Pro Asn Thr Leu Asp Pro Ile Phe Gly Met Met Phe Glu Leu Thr Cys
        275                 280                 285

Asn Ile Pro Leu Glu Lys Asp Leu Glu Ile Gln Leu Tyr Asp Phe Asp
    290                 295                 300

Leu Phe Ser Pro Asp Asp Lys Ile Gly Thr Thr Val Ile Asp Leu Glu
305                 310                 315                 320

Asn Arg Leu Leu Ser Gly Phe Gly Ala His Cys Gly Leu Ser Lys Ser
                325                 330                 335

Tyr Cys Gln Ser Gly Pro Phe Arg Trp Arg Asp Gln Met Pro Pro Ser
            340                 345                 350

Tyr Leu Leu Glu Arg Tyr Ala Lys Arg Lys Gly Leu Pro Pro Pro Leu
        355                 360                 365

Phe Ser Pro Glu Glu Asp Ala Val Phe Tyr Asn Gly Lys Lys Phe Lys
    370                 375                 380

Leu Gln Ser Phe Glu Pro Lys Thr Pro Thr Val His Gly Leu Gly Pro
385                 390                 395                 400

Lys Lys Glu Arg Leu Ala Leu Tyr Leu Leu His Thr Gln Gly Leu Val
                405                 410                 415

Pro Glu His Val Glu Thr Arg Thr Leu Tyr Ser His Ser Gln Pro Gly
            420                 425                 430

Ile Asp Gln Gly Lys Val Gln Met Trp Val Asp Ile Phe Pro Lys Lys
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435 440 445

Leu Gly Pro Pro Gly Pro Gln Val Asn Ile Asn Pro Arg Lys Pro Lys
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Arg Tyr Glu Leu Arg Cys Ile Ile Trp Lys Thr Ala Asn Val Asp Leu
465 470 475 480

Val Asp Asp Asn Leu Ser Arg Glu Lys Thr Ser Asp Ile Tyr Ile Lys
485 490 495

Gly Trp Leu Tyr Gly Leu Glu Lys Asp Met Gln Lys Thr Asp Ile His
500 505 510

Tyr His Ser Leu Thr Gly Glu Ala Asp Phe Asn Trp Arg Phe Ile Phe
515 520 525

Thr Met Asp Tyr Leu Ala Ala Glu Arg Thr Cys Val Gln Ser Gln Lys
530 535 540

Asp Tyr Ile Trp Ser Leu Asp Ala Thr Ser Met Lys Phe Pro Ala Arg
545 550 555 560

Leu Ile Ile Gln Val Trp Asp Asn Asp Ile Phe Ser Pro Asp Asp Phe
565 570 575

Leu Gly Val Leu Glu Leu Asp Leu Ser Asp Met Pro Leu Pro Ala Arg
580 585 590

His Ala Lys Gln Cys Ser Ile Arg Met Met Asp Ala Asp Pro Lys Trp
595 600 605

Pro Tyr Phe Ile Gln Tyr Lys His Phe Ser Leu Phe Lys Lys Lys Thr
610 615 620

Val Thr Gly Trp Trp Pro Cys Gln Val Leu Asp Gly Gly Lys Trp Arg
625 630 635 640

Leu Ser Gly Lys Val Lys Met Ser Leu Glu Ile Leu Ser Glu Lys Glu
645 650 655

Ala Leu Ile Lys Pro Ala Gly Arg Gly Gln Ser Glu Pro Asn Gln Tyr
660 665 670

Pro Thr Leu His Pro Pro Leu Arg Thr Asn Thr Ser Phe Thr Trp Leu
675 680 685

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Arg Ser Pro Val Gln Asn Phe Cys Tyr Ile Phe Trp Lys Arg Tyr Arg
    690                 695                 700

Phe Lys Leu Ile Ala Phe Met Val Ile Ser Ile Ile Ala Leu Met Leu
705                 710                 715                 720

Phe Asn Phe Ile Tyr Ser Ala Pro His Tyr Leu Ala Met Ser Trp Ile
                725                 730                 735

Lys Pro Gln Leu Gln Leu Tyr Pro Pro Ile Lys Ile Phe Asn Ile Ile
            740                 745                 750

Asn Ser Leu Asn Thr Ser Asn Ala Ser Ser Ser Ile Leu Pro Thr Gln
        755                 760                 765

Asp Pro Asn Leu Lys Pro Thr Ile Asp His Glu Trp Lys Leu His Pro
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Gly Pro Thr Asn His Leu Ser Asp Ile Phe Pro Glu Leu Pro Ala Pro
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<400> 82

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Leu Asp Ser Asn Arg Leu Ala Glu Val Arg Gly Asp Gln Leu Arg Gly
35 40 45

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Leu Gly Asn Leu Arg His Leu Ile Leu Gly Asn Asn Gln Ile Arg Arg
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Val Glu Ser Ala Ala Phe Asp Ala Phe Leu Ser Thr Val Glu Asp Leu
65                  70                  75                  80

Asp Leu Ser Tyr Asn Asn Leu Glu Ala Leu Pro Trp Glu Ala Val Gly
                85                  90                  95

Gln Met Val Asn Leu Asn Thr Leu Thr Leu Asp His Asn Leu Ile Asp
            100                 105                 110

His Ile Ala Glu Gly Thr Phe Val Gln Leu His Lys Leu Val Arg Leu
        115                 120                 125

Asp Met Thr Ser Asn Arg Leu His Lys Leu Pro Pro Asp Gly Leu Phe
    130                 135                 140

Leu Arg Ser Gln Gly Thr Gly Pro Lys Pro Pro Thr Pro Leu Thr Val
145                 150                 155                 160

Ser Phe Gly Gly Asn Pro Leu His Cys Asn Cys Glu Leu Leu Trp Leu
                165                 170                 175

Arg Arg Leu Thr Arg Glu Asp Asp Leu Glu Thr Cys Ala Thr Pro Glu
            180                 185                 190

His Leu Thr Asp Arg Tyr Phe Trp Ser Ile Pro Glu Glu Glu Phe Leu
        195                 200                 205

Cys Glu Pro Pro Leu Ile Thr Arg Gln Ala Gly Gly Arg Ala Leu Val
    210                 215                 220

Val Glu Gly Gln Ala Val Ser Leu Arg Cys Arg Ala Val Gly Asp Pro
225                 230                 235                 240

Glu Pro Val Val His Trp Val Ala Pro Asp Gly Arg Leu Leu Gly Asn
                245                 250                 255

Ser Ser Arg Thr Arg Val Arg Gly Asp Gly Thr Leu Asp Val Thr Ile
            260                 265                 270

Thr Thr Leu Arg Asp Ser Gly Thr Phe Thr Cys Ile Ala Ser Asn Ala
        275                 280                 285

Ala Gly Glu Ala Thr Ala Pro Val Glu Val Cys Val Val Pro Leu Pro
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290 295 300

Leu Met Ala Pro Pro Pro Ala Ala Pro Pro Pro Leu Thr Glu Pro Gly
305 310 315 320

Ser Ser Asp Ile Ala Thr Pro Gly Arg Pro Gly Ala Asn Asp Ser Ala
325 330 335

Ala Glu Arg Arg Leu Val Ala Ala Glu Leu Thr Ser Asn Ser Val Leu
340 345 350

Ile Arg Trp Pro Ala Gln Arg Pro Val Pro Gly Ile Arg Met Tyr Gln
355 360 365

Val Gln Tyr Asn Ser Ser Val Asp Asp Ser Leu Val Tyr Arg Met Ile
370 375 380

Pro Ser Thr Ser Gln Thr Phe Leu Val Asn Asp Leu Ala Ala Gly Arg
385 390 395 400

Ala Tyr Asp Leu Cys Val Leu Ala Val Tyr Asp Asp Gly Ala Thr Ala
405 410 415

Leu Pro Ala Thr Arg Val Val Gly Cys Val Gln Phe Thr Thr Ala Gly
420 425 430

Asp Pro Ala Pro Cys Arg Pro Leu Arg Ala His Phe Leu Gly Gly Thr
435 440 445

Met Ile Ile Ala Ile Gly Gly Val Ile Val Ala Ser Val Leu Val Phe
450 455 460

Ile Val Leu Leu Met Ile Arg Tyr Lys Val Tyr Gly Asp Gly Asp Ser
465 470 475 480

Arg Arg Val Lys Gly Ser Arg Ser Leu Pro Arg Val Ser His Val Cys
485 490 495

Ser Gln Thr Asn Gly Ala Gly Thr Gly Ala Ala Gln Ala Pro Ala Leu
500 505 510

Pro Ala Gln Asp His Tyr Glu Ala Leu Arg Glu Val Glu Ser Gln Ala
515 520 525

Ala Pro Ala Val Ala Val Glu Ala Lys Ala Met Glu Ala Glu Thr Ala
530 535 540

Ser Ala Glu Pro Glu Val Val Leu Gly Arg Ser Leu Gly Gly Ser Ala
545 550 555 560

Thr Ser Leu Cys Leu Leu Pro Ser Glu Glu Thr Ser Gly Glu Glu Ser
565 570 575

Arg Ala Ala Val Gly Pro Arg Arg Ser Arg Ser Gly Ala Leu Glu Pro
580 585 590

Pro Thr Ser Ala Pro Pro Thr Leu Ala Leu Val Pro Gly Gly Ala Ala
595 600 605

Ala Arg Pro Arg Pro Gln Gln Arg Tyr Ser Phe Asp Gly Asp Tyr Gly
610 615 620

Ala Leu Phe Gln Ser His Ser Tyr Pro Arg Arg Ala Arg Arg Thr Lys
625 630 635 640

Arg His Arg Ser Thr Pro His Leu Asp Gly Ala Gly Gly Gly Ala Ala
645 650 655

Gly Glu Asp Gly Asp Leu Gly Leu Gly Ser Ala Arg Ala Cys Leu Ala
660 665 670

Phe Thr Ser Thr Glu Trp Met Leu Glu Ser Thr Val
675 680

<210> 83
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 83
cgaactccgt gctcatc 17

<210> 84
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 84
cgcacaagtc gtaggca 17

<210> 85
<211> 2206

<212> DNA
<213> Homo sapiens

<400> 85
cgacaacgtc acccgcagac cggccaatcc cgccaggccg cggcccagtg gcgccggcgc 60

acaccgaaga cgacaccagc catccggcca atcccgcccc gccgcgcccc gcaggcccgc 120

ccactcctcg cttctccact tcccttctcg aagtgtccgg tcgcttctcg caggcggcgc 180

gcttgctggg tcacagtgag gcggctccgc gcaggcgcag ccgggcgggc gaggagcggg 240

gaagctgact cagggctgcg gccggggtcc tgcggggtag gagcgcgagg ccggcctgag 300

ggaggaggcc tagcgaccca tccggcgcct cccgccccgg gcacccgccc gcggccgcgc 360

atcctgcggg ccccaggagg cctccatctc aaaacaacgt gtttttagga tctcatccac 420

tatcacagtt tcagctttcc ccaaactgga atgtgtcttt gcagacgccc atccttatta 480

aagggcaaag acttctcata cacctaggat ggatcttata ttcttggcgg gactgcagag 540

aaggtgccgt gtcctgagtc ctcatgtcag ggcacaggct tccagccagt tctacctggg 600

ttatgtttat ctcaattccc tggtggtatt ggtgtctgct gggttttgcc agaatgaaga 660

caccgtgttt tcatttgtca gttgattcgt attttccagg aagacattct gagattacag 720

cattgtctta gtcaaggtgc tgcagaagga cagaactaat aggatatatg tacatatgaa 780

agaaagttta tgaagaactg gctcacacca tcacaaggca aagtcccatg acaggccatc 840

tgcaagctga ggagcgagga agccagcagt ggctcagccg gagtccaaca gcctcaaacg 900

gaatccaaca gttcaggctt cagtctgtgg ccaaatgccc agagaccccg gaaagctact 960

ggtgttagtc ccagagccgg aaggccaaag aacctggagt gtgatgtcca agggcaggag 1020

gaatggacag aagcatccag catggggtaa agacgaaagc cagaagactc agcaagctag 1080

cttacctact ttcttctgcc tgccttgttc tagccgcgct ggcagccggt tggagggtgc 1140

ccacccccac tgagggtgga tcttcctctc ctagtccact gactcaaatt tcagtctctc 1200

tgggagcacc atcacaccag aaacaatacc agccatctag ccacccttca gttcaccatc 1260

acaaccattg tcttattcat gaaacttctg cagacccacc ttaacctcca tcggtgactt 1320

ctacctgaag ccctctgatt gttgcccagt ggtgcttttt aaaataattt ccatagtttc 1380

ttctacacct ttagttggca ttctactgta aaggagagat tttatttttct tactcattta 1440

tttgttagtt tatagtcacc accatatgga tgcagagttc tgtctcattc actgggaagt 1500

attctattgc agtcatgatt tattttgatg ttcacatccc agagttggtg agtgagcgcc 1560

ccttcacgct ggctcccgag tgctgacgtg tccccgtcct tctctgcact tttccttacc 1620

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catctcccta gggacgttgg ttcctttatg gaaggtggca tttagaagcc aggatttggg 1740

ctgagcactg tggctcatgc ttgtaatccc agcacttggg gaggccgaag tgggcggatc 1800

gctggaggcc aagagtctga gaccagcctg gctaacatgg tgaaaccctt ccccgtctct 1860

actacaaata aaaaattagc tgggtgtgtt ggcacgtgcc tgtaatccca gttactcagg 1920

aggctgaagc accagaatct cttgaaccca ggaggccgag gttgcagtga gccaagattg 1980

caccactgca ctacagcttg ggtgacagcg cgagacaccg tctcaaaaag gataataatt 2040

taaaaaacag caggatttgg gtgagcagtg cgctcattgc ttctgggctc tctcggtgga 2100

cataggctag gaatgtaaga tgtatgtgcc tgtgtatata cacacgtctg tagctatgtc 2160

tatgttgcat acatgtgttt ttccaaaaac caaatccata accatg 2206

<210> 86
<211> 93
<212> PRT
<213> Homo sapiens

<400> 86

Met Asp Arg Ser Ile Gln His Gly Val Lys Thr Lys Ala Arg Arg Leu
1 5 10 15

Ser Lys Leu Ala Tyr Leu Leu Ser Ser Ala Cys Leu Val Leu Ala Ala
20 25 30

Leu Ala Ala Gly Trp Arg Val Pro Thr Pro Thr Glu Gly Gly Ser Ser
35 40 45

Ser Pro Ser Pro Leu Thr Gln Ile Ser Val Ser Leu Gly Ala Pro Ser
50 55 60

His Gln Lys Gln Tyr Gln Pro Ser Ser His Pro Ser Val His His His
65 70 75 80

Asn His Cys Leu Ile His Glu Thr Ser Ala Asp Pro Pro
85 90

<210> 87
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 87
aaactacgtg tggccaggat c 21

<210> 88
<211> 21

<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 88
cgacatgagg actcaggaca c 21

<210> 89
<211> 455
<212> DNA
<213> Homo sapiens

<400> 89
gtgaagacag ggagctcaag tgacctcctc cagggtatat agctgtggtg tgggaagcat 60

catgagaaca cggtctttga tggggataat tactctgaat ctaccaggct gattaagcca 120

cagcagatca gcaggtgaga attcaactgt ccagatagaa aggtggacat ggaaaaattg 180

ggctttgcaa atggtcaccc aattcttgcc ttcctggtct ccagatcacc cttcctatac 240

cgccactctg gagaaagaag tacagaacgc taacaaggat ggcttggagt tgcagtggtc 300

acctcagatc ttaaggtcac tttggagatg gaacccctgt gactaggaat ggcagaagag 360

aaaggtagaa agagattgag tcctggggat gtggcagagc accatcctag ccccgtactg 420

cgtacttctg gacttccttt aaattgagag aaaca 455

<210> 90
<211> 61
<212> PRT
<213> Homo sapiens

<400> 90

Cys Phe Ser Gln Phe Lys Gly Ser Pro Glu Val Arg Ser Thr Gly Leu
1 5 10 15

Gly Trp Cys Ser Ala Thr Ser Pro Gly Leu Asn Leu Phe Leu Pro Phe
20 25 30

Ser Ser Ala Ile Pro Ser His Arg Gly Ser Ile Ser Lys Val Thr Leu
35 40 45

Arg Ser Glu Val Thr Thr Ala Thr Pro Ser His Pro Cys
50 55 60

<210> 91
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 91
gaacacggtc tttgatgggg 20

<210> 92
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 92
gccatccttg ttagcgttct g 21

<210> 93
<211> 1230
<212> DNA
<213> Homo sapiens

<400> 93
aggggcagag gggtcttccc aaccctaccc ctattttcgg tgatttttgt gtgagaatat 60

taatattaaa aataaacgga gaaaaaaaat cctgtttcgc taacggctgg tggtagcagg 120

ttgagtaccg ggagggctgc aagaccgtga ttgatgggga ggactgcgca gaccctggcg 180

agggtgagcc cctccccgga ggcgcctgtg gaatgtccag ggctctggtc cgctcctcgg 240

gatgggggt gcctaatcct agagccgcat tccaggataa ggggggtggg gagaggctgg 300

gccgggggag gggcaggaaa gagggctata agggcagcgg cccaggcggg cgggatccag 360

gcgggccatg gcggatgtcc ccggggcaca gcgagcggtt cctggtgacg gcccagagcc 420

ccgggacccc ctggactgtt gggcctgcgc tgttcttgta acagcccaga atctgctggt 480

ggctgccttc aatcttctcc tgctggtgct ggtgctaggg accatcttgc tacccgctgt 540

caccatgctg ggcttcggct tcctctgcca ctctcagttc ctgcgctccc aggcaccccc 600

ttgcaccgcg cacctgcggg accccggttt cacggcccta ctggtcaccg gattcctgct 660

cctcgtgccg ctgctcgtgc ttgctctggc cagctaccgc cgcctctgcc tgcgcctccg 720

cctagccgat tgcctcgtgc cctacagccg agcccttat cggcgtcggc gcgccccgca 780

gccgcggcaa atccgggcct caccagggtc ccaggccgtt cccacatcag gaaaggtctg 840

ggtctaatga ccctcgagtc aagaacaacc ctgacggctg ccctccctct tattcggccc 900

aaggacttga agcccggcat cttccgacct gccctgcccc cacccctgcc tgagcggagt 960

cctagcatcc ccttgggagc agcagcgtca gtggacccag tgctgagaaa agcccccaca 1020

tcccggaaaa cccactttcc tttcacgacc cacatctcaa tcctgaacat ctaggctgga 1080

acctgcacac ctccccctca gctccgtcgt gaatgggaca acaatctcgt gccctcgttt 1140

tatggtgcag cttctctagt atttctgggg ctgggggcg gggctggagg ggaaggagtg 1200

tccacgcatc aataaagatt taacgaactg 1230

<210> 94
<211> 159
<212> PRT
<213> Homo sapiens

<400> 94

Met Ala Asp Val Pro Gly Ala Gln Arg Ala Val Pro Gly Asp Gly Pro
1 5 10 15

Glu Pro Arg Asp Pro Leu Asp Cys Trp Ala Cys Ala Val Leu Val Thr
20 25 30

Ala Gln Asn Leu Leu Val Ala Ala Phe Asn Leu Leu Leu Leu Val Leu
35 40 45

Val Leu Gly Thr Ile Leu Leu Pro Ala Val Thr Met Leu Gly Phe Gly
50 55 60

Phe Leu Cys His Ser Gln Phe Leu Arg Ser Gln Ala Pro Pro Cys Thr
65 70 75 80

Ala His Leu Arg Asp Pro Gly Phe Thr Ala Leu Leu Val Thr Gly Phe
85 90 95

Leu Leu Leu Val Pro Leu Leu Val Leu Ala Leu Ala Ser Tyr Arg Arg
100 105 110

Leu Cys Leu Arg Leu Arg Leu Ala Asp Cys Leu Val Pro Tyr Ser Arg
115 120 125

Ala Leu Tyr Arg Arg Arg Arg Ala Pro Gln Pro Arg Gln Ile Arg Ala
130 135 140

Ser Pro Gly Ser Gln Ala Val Pro Thr Ser Gly Lys Val Trp Val
145 150 155

<210> 95
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 95
ttcctctgcc actctcagtt c 21

<210> 96
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 96
cgataaaggg ctcggctgta g 21

<210> 97
<211> 1020
<212> DNA
<213> Homo sapiens

<400> 97
atggaggagg aggaggagga tgatgactat gagaactcaa cacctcccta caaggacctt 60

cctcccaagc cagggaccat ggaggaggag gaggaggatg atgactatga gaactcaaca 120

cctccctaca aggaccttcc tcccaagcca gggaccatgg aggaggagga ggaggatgat 180

gactatgaga actcaacacc tccctacaag gaccttcctc ccaagccagg ttcaagtgct 240

ccaccaagac ctccaagggc agcaaaggaa acagagaaac ccccacttcc ttgcaagccc 300

cggaacatga caggcctgga cctcgccgct gtcacctgtc cacctcctca actggctgtg 360

aatcttgagc cttctccatt gcagccatcc ctggccgcaa ctccagtccc ctggctcaat 420

cagaggtctg gaggtcctgg ctgctgccag aagaggtgga tggtgtacct gtgtctgctg 480

gtggtgactt ccctgttcct gggctgcctt ggtctcactg tgaccctgat taagttgact 540

ggcatggcag ggctagctgg cctgaagcat gacattgccc gtgtaagagc tgacaccaac 600

cagtccctgg tggaactttg gggcttatta gactgccgcc gaattacctg tcctgaaggc 660

tggctgccct ttgagggcaa gtgttactac ttctccccaa gcaccaagtc atgggatgag 720

gcccggatgt tctgccagga gaattactct cacttggtca tcatcaatag ctttgctgag 780

cacaattttg tggccaaggc ccatggctct ccacgggtgt actggctggg gctgaatgac 840

agggcccagg aaggggactg gaggtggctg gatgggtctc ctgtgacatt aaggcaacca 900

gaggaaccca ataacatcca cgatgaggac tgtgctacca tgaacaaagg tggcacctgg 960

aatgatctct cttgctacaa aactacgtat tggatttgtg agcggaaatg ttcctgttga 1020

<210> 98
<211> 339
<212> PRT
<213> Homo sapiens

<400> 98

Met Glu Glu Glu Glu Glu Asp Asp Asp Tyr Glu Asn Ser Thr Pro Pro

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1               5                   10                  15

Tyr Lys Asp Leu Pro Pro Lys Pro Gly Thr Met Glu Glu Glu Glu Glu
            20                  25                  30

Asp Asp Asp Tyr Glu Asn Ser Thr Pro Pro Tyr Lys Asp Leu Pro Pro
        35                  40                  45

Lys Pro Gly Thr Met Glu Glu Glu Glu Glu Asp Asp Asp Tyr Glu Asn
    50                  55                  60

Ser Thr Pro Pro Tyr Lys Asp Leu Pro Pro Lys Pro Gly Ser Ser Ala
65                  70                  75                  80

Pro Pro Arg Pro Pro Arg Ala Ala Lys Glu Thr Glu Lys Pro Pro Leu
                85                  90                  95

Pro Cys Lys Pro Arg Asn Met Thr Gly Leu Asp Leu Ala Ala Val Thr
            100                 105                 110

Cys Pro Pro Pro Gln Leu Ala Val Asn Leu Glu Pro Ser Pro Leu Gln
        115                 120                 125

Pro Ser Leu Ala Ala Thr Pro Val Pro Trp Leu Asn Gln Arg Ser Gly
    130                 135                 140

Gly Pro Gly Cys Cys Gln Lys Arg Trp Met Val Tyr Leu Cys Leu Leu
145                 150                 155                 160

Val Val Thr Ser Leu Phe Leu Gly Cys Leu Gly Leu Thr Val Thr Leu
                165                 170                 175

Ile Lys Leu Thr Gly Met Ala Gly Leu Ala Gly Leu Lys His Asp Ile
            180                 185                 190

Ala Arg Val Arg Ala Asp Thr Asn Gln Ser Leu Val Glu Leu Trp Gly
        195                 200                 205

Leu Leu Asp Cys Arg Arg Ile Thr Cys Pro Glu Gly Trp Leu Pro Phe
    210                 215                 220

Glu Gly Lys Cys Tyr Tyr Phe Ser Pro Ser Thr Lys Ser Trp Asp Glu
225                 230                 235                 240

Ala Arg Met Phe Cys Gln Glu Asn Tyr Ser His Leu Val Ile Ile Asn
                245                 250                 255
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Ser Phe Ala Glu His Asn Phe Val Ala Lys Ala His Gly Ser Pro Arg
260 265 270

Val Tyr Trp Leu Gly Leu Asn Asp Arg Ala Gln Glu Gly Asp Trp Arg
275 280 285

Trp Leu Asp Gly Ser Pro Val Thr Leu Arg Gln Pro Glu Glu Pro Asn
290 295 300

Asn Ile His Asp Glu Asp Cys Ala Thr Met Asn Lys Gly Gly Thr Trp
305 310 315 320

Asn Asp Leu Ser Cys Tyr Lys Thr Thr Tyr Trp Ile Cys Glu Arg Lys
325 330 335

Cys Ser Cys

<210> 99
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 99
atagctttgc tgagcacctt c 21

<210> 100
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 100
aagagacact cagatatgga c 21

<210> 101
<211> 1680
<212> DNA
<213> Homo sapiens

<400> 101
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ctgcggattt tatatggtgt gctcttccta ctgatttacc tggcagccct aatgagtaac 120

cttctcatca ttactctcat taccctggac gtaaagctcc aaacacccat gtacttcttc 180

ctgaagaact tatccttttt ggatgtcttc ctggtgtctg ttccaatccc aaaattcatt 240

gtcaacaacc taacccacaa caattccatt tccattctag gatgtgcctt ccagctactt 300

ttaatgactt ccttctcagc aggagagata tttatcctca ctgccatgtc ctatgaccgc 360

tatgtagcca tctgctgtcc cctgaactac gaggtaatca tgaatactgg agtctgtgtg 420

ttaatggcaa gtgtttcctg ggccattgga gggctctttg gtactgcgta cacagctggc 480

acattttcca tgcctttctg tggctccagt gtgattccac agtttttctg tgatgttcct 540

tcattactaa ggatttcctg ttctgaaaca ctaatggtaa tttatgcagg tattggagtt 600

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tccactgtac tgaagatccc taccactaaa ggactgtgtg attgggttaa agggctcagt 720

gcggggactc tgttttctgg tttcagtacc acaatggaca caggcaacaa aactctgccc 780

caggactttc tcttactggg ctttcctggt tctcaaactc ttcagctctc tctctttatg 840

ctttttctgg tgatgtacat cctcacagtt agtggtaatg tggctatctt gatgttggtg 900

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gagatttggt ataccacagc agcagtgccc aaagcactgg ccatcctact ggggagaagt 1020

cagaccatat catttacaag ctgtcttttg cagatgtact ttgttttctc attaggctgc 1080

acagagtact tcctcctggc agccatggct tatgaccgct gtcttgccat ctgctatcct 1140

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atttggtatg ggtccacagt tttccttcac gtccgcacct ctatcaaaga tgccttggat 1560

ctgatcaaag ctgtccacgt cctgaacact gtggtgactc cagttttaaa ccccttcatc 1620

tatacgcttc gtaataagga agtaagagag actctgctga agaaatggaa gggaaaataa 1680

<210> 102
<211> 559
<212> PRT
<213> Homo sapiens

<400> 102

Met Ala Asn Val Thr Leu Val Thr Gly Phe Leu Leu Met Gly Phe Ser
1 5 10 15

Asn Ile Gln Lys Leu Arg Ile Leu Tyr Gly Val Leu Phe Leu Leu Ile
20 25 30

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Tyr Leu Ala Ala Leu Met Ser Asn Leu Leu Ile Ile Thr Leu Ile Thr
        35                  40                  45

Leu Asp Val Lys Leu Gln Thr Pro Met Tyr Phe Phe Leu Lys Asn Leu
    50                  55                  60

Ser Phe Leu Asp Val Phe Leu Val Ser Val Pro Ile Pro Lys Phe Ile
65                  70                  75                  80

Val Asn Asn Leu Thr His Asn Asn Ser Ile Ser Ile Leu Gly Cys Ala
                85                  90                  95

Phe Gln Leu Leu Leu Met Thr Ser Phe Ser Ala Gly Glu Ile Phe Ile
            100                 105                 110

Leu Thr Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu
        115                 120                 125

Asn Tyr Glu Val Ile Met Asn Thr Gly Val Cys Val Leu Met Ala Ser
    130                 135                 140

Val Ser Trp Ala Ile Gly Gly Leu Phe Gly Thr Ala Tyr Thr Ala Gly
145                 150                 155                 160

Thr Phe Ser Met Pro Phe Cys Gly Ser Ser Val Ile Pro Gln Phe Phe
                165                 170                 175

Cys Asp Val Pro Ser Leu Leu Arg Ile Ser Cys Ser Glu Thr Leu Met
            180                 185                 190

Val Ile Tyr Ala Gly Ile Gly Val Gly Ala Cys Leu Ser Ile Ser Cys
        195                 200                 205

Phe Ile Cys Ile Val Ile Ser Tyr Ile Tyr Ile Phe Ser Thr Val Leu
    210                 215                 220

Lys Ile Pro Thr Thr Lys Gly Leu Cys Asp Trp Val Lys Gly Leu Ser
225                 230                 235                 240

Ala Gly Thr Leu Phe Ser Gly Phe Ser Thr Thr Met Asp Thr Gly Asn
                245                 250                 255

Lys Thr Leu Pro Gln Asp Phe Leu Leu Leu Gly Phe Pro Gly Ser Gln
            260                 265                 270

Thr Leu Gln Leu Ser Leu Phe Met Leu Phe Leu Val Met Tyr Ile Leu
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275 280 285

Thr Val Ser Gly Asn Val Ala Ile Leu Met Leu Val Ser Thr Ser His
290 295 300

Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu
305 310 315 320

Glu Ile Trp Tyr Thr Thr Ala Ala Val Pro Lys Ala Leu Ala Ile Leu
325 330 335

Leu Gly Arg Ser Gln Thr Ile Ser Phe Thr Ser Cys Leu Leu Gln Met
340 345 350

Tyr Phe Val Phe Ser Leu Gly Cys Thr Glu Tyr Phe Leu Leu Ala Ala
355 360 365

Met Ala Tyr Asp Arg Cys Leu Ala Ile Cys Tyr Pro Leu His Tyr Gly
370 375 380

Ala Ile Met Ser Ser Leu Leu Ser Ala Gln Leu Ala Leu Gly Ser Trp
385 390 395 400

Val Cys Gly Phe Val Ala Ile Ala Val Pro Thr Ala Leu Ile Ser Gly
405 410 415

Leu Ser Phe Cys Gly Pro Arg Ala Ile Asn His Phe Phe Cys Asp Ile
420 425 430

Ala Pro Trp Ile Ala Leu Ala Cys Thr Asn Thr Gln Ala Val Glu Leu
435 440 445

Val Ala Phe Val Ile Ala Val Val Val Ile Leu Ser Ser Cys Leu Ile
450 455 460

Thr Phe Val Ser Tyr Val Tyr Ile Ile Ser Thr Ile Leu Arg Ile Pro
465 470 475 480

Ser Ala Ser Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser His Leu
485 490 495

Thr Val Val Leu Ile Trp Tyr Gly Ser Thr Val Phe Leu His Val Arg
500 505 510

Thr Ser Ile Lys Asp Ala Leu Asp Leu Ile Lys Ala Val His Val Leu
515 520 525

Asn Thr Val Val Thr Pro Val Leu Asn Pro Phe Ile Tyr Thr Leu Arg
530 535 540

Asn Lys Glu Val Arg Glu Thr Leu Leu Lys Lys Trp Lys Gly Lys
545 550 555

<210> 103
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 103
catttcttgt ttcatctgta ttgtg 25

<210> 104
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 104
tgttgcctgt gtccattgtg 20

<210> 105
<211> 499
<212> DNA
<213> Homo sapiens

<400> 105
acacccacat ggtcggcgtg caggatattt cgctggaccc tagaaaagcc accacgacct 60

gtgggccatg atgctacccc aatggctgct gctgctgttc cttctcttct tctttctctt 120

cctcctcacc aggggctcac tttctccaac aaaatacaac cttttggagc tcaaggagtc 180

ttgcatccgg aaccaggact gcgagactgg ctgctgccaa cgtgctccag acaattgcga 240

gtcgcactgc gcggagaagg ggtccgaggg cagtctgtgt caaacgcagg tgttctttgg 300

ccaatataga gcgtgtccct gcctgcggaa cctgacttgt atatattcaa agaatgagaa 360

atggcttagc atcgcctatg gccgttgtca gaaaattgga aggcagaagt tggctaagaa 420

aatgttcttc tagtgctccc tccttcttgc tgcctcctcc tcctccacct gctctcctcc 480

ctacccagag ctctgtgtt 499

<210> 106
<211> 121
<212> PRT
<213> Homo sapiens

<400> 106

Met Met Leu Pro Gln Trp Leu Leu Leu Leu Phe Leu Leu Phe Phe Phe
1 5 10 15

Leu Phe Leu Leu Thr Arg Gly Ser Leu Ser Pro Thr Lys Tyr Asn Leu
20 25 30

Leu Glu Leu Lys Glu Ser Cys Ile Arg Asn Gln Asp Cys Glu Thr Gly
35 40 45

Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His Cys Ala Glu Lys
50 55 60

Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Val Phe Phe Gly Gln Tyr
65 70 75 80

Arg Ala Cys Pro Cys Leu Arg Asn Leu Thr Cys Ile Tyr Ser Lys Asn
85 90 95

Glu Lys Trp Leu Ser Ile Ala Tyr Gly Arg Cys Gln Lys Ile Gly Arg
100 105 110

Gln Lys Leu Ala Lys Lys Met Phe Phe
115 120

<210> 107
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 107
tgtgtcaaac gcaggtg 17

<210> 108
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 108
ggagggagca ctagaagaac 20

<210> 109
<211> 659
<212> DNA
<213> Homo sapiens

<400> 109
agcaaattac accattaatg tcatcctggc gaatgaaaca agagaatagt atttatcaga 60

gaaagtctgg tgagttgaag tccaagaccc caggaaacaa ctagccctgc tgggctgccc 120

ctccttcgga gtgggactat atgatcctca tcaggccaat ccacgtcaca gaatggtcta 180

ggcattggat gagtgcctca atctgagcca atgaaggtca ttgctgagac attttactgg 240

ttgccaggct gcaggcatcc caggcttcct gctgccctca tgtctacaac ctgtcgtctg 300

gaacattcca ggagccactt ttatcacttg cagcaatctt cttcagtgag ttccccagga 360

cttgatttca tcttacaatc tgattccatg tgtctcccat attttaagga ttctttatta 420

tttctggctt acagagaaca aacattattt tttgctttcc tggtctgttc tagattttca 480

aaaataactc tgtcacttct gttatatggt atcattgctt gtaattatct atttacttat 540

ctgtctctgg actggactct ttacagacag gcaataacta attatctgtc tgtctggcat 600

ttggtagtca ctcataaatc gtttattgca ttactaacta aataaaaaag ttgaccttg 659

<210> 110
<211> 144
<212> PRT
<213> Homo sapiens

<400> 110

Met Lys Val Ile Ala Glu Thr Phe Tyr Trp Leu Pro Gly Cys Arg His
1 5 10 15

Pro Arg Leu Pro Ala Ala Leu Met Ser Thr Thr Cys Arg Leu Glu His
20 25 30

Ser Arg Ser His Phe Tyr His Leu Gln Gln Ser Ser Ser Val Ser Ser
35 40 45

Pro Gly Leu Asp Phe Ile Leu Gln Ser Asp Ser Met Cys Leu Pro Tyr
50 55 60

Phe Lys Asp Ser Leu Leu Phe Leu Ala Tyr Arg Glu Gln Thr Leu Phe
65 70 75 80

Phe Ala Phe Leu Val Cys Ser Arg Phe Ser Lys Ile Thr Leu Ser Leu
85 90 95

Leu Leu Tyr Gly Ile Ile Ala Cys Asn Tyr Leu Phe Thr Tyr Leu Ser
100 105 110

Leu Asp Trp Thr Leu Tyr Arg Gln Ala Ile Thr Asn Tyr Leu Ser Val
115 120 125

Trp His Leu Val Val Thr His Lys Ser Phe Ile Ala Leu Leu Thr Lys
130 135 140

<210> 111
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 111
atcctggcga atgaaacaag agaat 25

<210> 112
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 112
gcaaccagta aaatgtctca gcaatg 26

<210> 113
<211> 831
<212> DNA
<213> Homo sapiens

<400> 113
atgcgaagaa agaacctcac agaggtaaca gagtttgttt tcctgggatt ctccagattc 60

cacaaacatc acatcactct ctttgtggtt tttctcatcc tgtacacatt aactgtggct 120

ggcaatgcca tcatcatgac catcatctgc attgaccgtc acctccacac tcccatgtac 180

ttcttcctga gcatgctggc tagctcaaag acagtgtaca cactgttcat cattccacag 240

atgctctcca gcttcgtaac ccagacccag ccaatctccc tagcaggttg taccacccaa 300

acgttcttct ttgttacctt ggccatcaac aattgcttct tgctcacagt gatgggctat 360

gaccactata tggccatctg caatcccttg agatacaggg tcattacgag caagaaggtg 420

tgtgtccagc tggtgtgtgg agcctttagc attggcctgg ccatggcagc tgtccaggta 480

acatccatat ttaccttacc tttttgtcac acggtggttg gtcatttctt ctgtgacatc 540

ctccctgtca tgaaactctc ctgtattaat accactatca atgagataat caattttgtt 600

gtcaggttat ttgtcatcct ggtccccatg ggtctggtct tcatctccta tgtcctcatc 660

atctccactg tcctcaagat tgcctcagct gagggttgga agaagacctt tgccacctgt 720

gccttccacc tcactgtggt cattgtccat tatggctgtg cttccattgc ctacctcatg 780

cccaagtcag aaaactctat agaacaagac ctccttctct cagtgaccta a 831

<210> 114
<211> 276
<212> PRT
<213> Homo sapiens

<400> 114

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Met Arg Arg Lys Asn Leu Thr Glu Val Thr Glu Phe Val Phe Leu Gly
1               5                  10                  15

Phe Ser Arg Phe His Lys His His Ile Thr Leu Phe Val Val Phe Leu
            20                  25                  30

Ile Leu Tyr Thr Leu Thr Val Ala Gly Asn Ala Ile Ile Met Thr Ile
        35                  40                  45

Ile Cys Ile Asp Arg His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
    50                  55                  60

Met Leu Ala Ser Ser Lys Thr Val Tyr Thr Leu Phe Ile Ile Pro Gln
65                  70                  75                  80

Met Leu Ser Ser Phe Val Thr Gln Thr Gln Pro Ile Ser Leu Ala Gly
                85                  90                  95

Cys Thr Thr Gln Thr Phe Phe Phe Val Thr Leu Ala Ile Asn Asn Cys
            100                 105                 110

Phe Leu Leu Thr Val Met Gly Tyr Asp His Tyr Met Ala Ile Cys Asn
        115                 120                 125

Pro Leu Arg Tyr Arg Val Ile Thr Ser Lys Lys Val Cys Val Gln Leu
    130                 135                 140

Val Cys Gly Ala Phe Ser Ile Gly Leu Ala Met Ala Ala Val Gln Val
145                 150                 155                 160

Thr Ser Ile Phe Thr Leu Pro Phe Cys His Thr Val Val Gly His Phe
                165                 170                 175

Phe Cys Asp Ile Leu Pro Val Met Lys Leu Ser Cys Ile Asn Thr Thr
            180                 185                 190

Ile Asn Glu Ile Ile Asn Phe Val Val Arg Leu Phe Val Ile Leu Val
        195                 200                 205

Pro Met Gly Leu Val Phe Ile Ser Tyr Val Leu Ile Ile Ser Thr Val
    210                 215                 220
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Leu Lys Ile Ala Ser Ala Glu Gly Trp Lys Lys Thr Phe Ala Thr Cys
225 230 235 240

Ala Phe His Leu Thr Val Val Ile Val His Tyr Gly Cys Ala Ser Ile
245 250 255

Ala Tyr Leu Met Pro Lys Ser Glu Asn Ser Ile Glu Gln Asp Leu Leu
260 265 270

Leu Ser Val Thr
275

<210> 115
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 115
cttcgtaacc cagaccca 18

<210> 116
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 116
cttgctcgta atgaccct 18

<210> 117
<211> 1233
<212> DNA
<213> Homo sapiens

<400> 117
gaagcagcca ccaccatctt gggagctctg ggagcaagga cccctgtaac acattcatcc 60

ttgaatgaca aaatgtctgg tccagcatgg tattataaca taaacatgaa gaggaagaga 120

catgagagat acgcacagtg aagagaccaa gctgggacac agtacgaagg tggcatctgc 180

acgccaagca gagggacctc agaagaaact gagccagcca gcaccccacc ttcgtctttg 240

acctccagcc tccagaacta aggatagagc tcttcatctc tgttagaaac gaccatcaaa 300

aagatacatc aattcattag aatcaaaagg acatgagtta tcagaattct ttctcctgaa 360

agaaagtgga gatcaaaggt aaaacttcta gagaatgaga tgaaggcaga tgaaagaagt 420

taacaagaca ttacatgact tgataatatt gcatgtatgc aaaaaccttа tgaaatcaac 480

tgtgttctag cgaccacttg tttttctttt tgtcataata ctttttattc tcttgcaatg 540

atattgattc atctgcacct gacatcaact ctgcatttgt agaaggtgat aagaatacag 600

ggaaatggaa taagtggctt tgcctgcaat cccgcagcag cagaaatgtc catttcctct 660

ctcctgaata atactacatt ctccactggg ttccacaagt ttcgaggtaa aagcatgaac 720

atacacgaag tcaccatcac taccctcacc accaccacca ttatttccac catattcacc 780

cttttaatac gcaaacttcc tccaaggctt cctgaagtca cccagaaatg catttcccca 840

agagtgagtt gtgctaacat tgtatcctat ggaactctgg gaagctaccc agatcctcaa 900

ctcttggagt cttgctgact gcatgttcca ggctccacat ttaagctcca gtgactgctg 960

atgactgcat gacctaacac atgtcctcaa tcctttcttg gcctcagttt cttcaccagt 1020

gaattctgaa tgctggaatt ggcaatattt caggttcttt ccaactggaa atacccatgc 1080

taataatttt agtaagtcaa tagccataga aacctactga caaaatgagt attttaacag 1140

agacagttgt actttcttaa tttttagcag aagggaatgc atatgtataa tatctatgtt 1200

gccttctatg tgtaaaaata aatacacaga cac 1233

<210> 118
<211> 90
<212> PRT
<213> Homo sapiens

<400> 118

Met Ser Ile Ser Ser Leu Leu Asn Asn Thr Thr Phe Ser Thr Gly Phe
1 5 10 15

His Lys Phe Arg Gly Lys Ser Met Asn Ile His Glu Val Thr Ile Thr
20 25 30

Thr Leu Thr Thr Thr Thr Ile Ile Ser Thr Ile Phe Thr Leu Leu Ile
35 40 45

Arg Lys Leu Pro Pro Arg Leu Pro Glu Val Thr Gln Lys Cys Ile Ser
50 55 60

Pro Arg Val Ser Cys Ala Asn Ile Val Ser Tyr Gly Thr Leu Gly Ser
65 70 75 80

Tyr Pro Asp Pro Gln Leu Leu Glu Ser Cys
85 90

<210> 119
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 119
caccccacct tcgtctttg 19

<210> 120
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 120
gttttacctt tgatctccac tttc 24

<210> 121
<211> 4209
<212> DNA
<213> Homo sapiens

<400> 121
agttgcttga aagcaacgtg cctattcaca tggagaatct tccctttcct ttaaaattac 60

ttagtgcctc atcgctaaac gcccccagct ccacaccatg ggtgttggat atcttcctca 120

ccttggtgtt tgccctgggg ttcttcttcc tattactccc ctacttatct tacttccatt 180

gtgatgaccc accctcacca tcgcctggga agagaaagtg tccagtaggg cggaggcgga 240

ggcccagagg caggatgaaa aaccacagtc tgagagctgg tagagagtgc ccgagaggcc 300

tggaggagac ttcggacctt ctttcacaac tgcagagcct cctggggcca caccttgaca 360

aaggtgactt tggtcagctc tccggtccag acccccccagg tgaggtgggc gaaagagcac 420

ctgatggagc ctcccagtcc tctcatgagc ctatggaaga tgctgctccc attctctccc 480

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caaatcaaat gaccccagaa aagcacttaa attctttggg gaatttggct aaatcattgg 1140

atgctgagca ggacaccaca aacccaaaac ccttctggaa catgggagag aactcgaaac 1200

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ccaaagcatc tgatcacatg ccagagagtc ttctggcctc ctcacctgca tggaagcagt 2700

tccagagggc accgcgagga atcccatctt ggaatgatca tgggcccttg aagcctcctc 2760

cagctggaca ggagggcagg tggccatcta agcccctcac gtacagcctc acaggcagca 2820

cccagcagag caggagctta ggagcccaat cttcaaaggc tggagagaca agggaggcag 2880

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aggatgtgca tggtttcgag gctccaggga ccagcaaaag ctctctacac cctagagtgt 3000

ctgtctccca agatccaaga aagctgtgtc ttatggagga ggttgttagt gaatttgagc 3060

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aacagcctcc ttcagtaagc cactttggag aaaacatcaa gcaatttttt cagtggattt 3540

tttcaaagaa aaaaagcaag ccagcaccag tcactgctga gagccaaaaa acagtaaaaa 3600

acagatcatg tgtgtacagc agcagtgctg aagctcaggg tctcatgacg gcagttggac 3660

aaatgctgga caagaaaatg tcactttgcc atgcgcacca tgcctcgaag gtaaatcagc 3720

acaaacagaa gtttcaagcc ccagtctgtg ggtttccctg caaccacagg cacctcttct 3780

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<210> 122
<211> 1343
<212> PRT
<213> Homo sapiens

<400> 122

Met Glu Asn Leu Pro Phe Pro Leu Lys Leu Leu Ser Ala Ser Ser Leu
1 5 10 15

Asn Ala Pro Ser Ser Thr Pro Trp Val Leu Asp Ile Phe Leu Thr Leu
20 25 30

Val Phe Ala Leu Gly Phe Phe Phe Leu Leu Leu Pro Tyr Leu Ser Tyr
35 40 45

```
Phe His Cys Asp Asp Pro Pro Ser Pro Ser Pro Gly Lys Arg Lys Cys
    50                  55                  60

Pro Val Gly Arg Arg Arg Arg Pro Arg Gly Arg Met Lys Asn His Ser
65                  70                  75                  80

Leu Arg Ala Gly Arg Glu Cys Pro Arg Gly Leu Glu Glu Thr Ser Asp
                85                  90                  95

Leu Leu Ser Gln Leu Gln Ser Leu Leu Gly Pro His Leu Asp Lys Gly
            100                 105                 110

Asp Phe Gly Gln Leu Ser Gly Pro Asp Pro Pro Gly Glu Val Gly Glu
        115                 120                 125

Arg Ala Pro Asp Gly Ala Ser Gln Ser Ser His Glu Pro Met Glu Asp
    130                 135                 140

Ala Ala Pro Ile Leu Ser Pro Leu Ala Ser Pro Asp Pro Gln Ala Lys
145                 150                 155                 160

His Pro Gln Asp Leu Ala Ser Thr Pro Ser Pro Gly Pro Met Thr Thr
                165                 170                 175

Ser Val Ser Ser Leu Ser Ala Ser Gln Pro Pro Glu Pro Ser Leu Pro
            180                 185                 190

Leu Glu His Pro Ser Pro Glu Pro Pro Ala Leu Phe Pro His Pro Pro
        195                 200                 205

His Thr Pro Asp Pro Leu Ala Cys Ser Pro Pro Pro Pro Lys Gly Phe
    210                 215                 220

Thr Ala Pro Pro Leu Arg Asp Ser Thr Leu Ile Thr Pro Ser His Cys
225                 230                 235                 240

Asp Ser Val Ala Leu Pro Leu Gly Thr Val Pro Gln Ser Leu Ser Pro
                245                 250                 255

His Glu Asp Leu Val Ala Ser Val Pro Ala Ile Ser Gly Leu Gly Gly
            260                 265                 270

Ser Asn Ser His Val Ser Ala Ser Ser Arg Trp Gln Glu Thr Ala Arg
        275                 280                 285

Thr Ser Cys Ala Phe Asn Ser Ser Val Gln Gln Asp Pro Leu Ser Arg
    290                 295                 300
```

```
His Pro Pro Glu Thr Cys Gln Met Glu Ala Gly Ser Leu Phe Leu Leu
305                 310                 315                 320

Ser Ser Asp Gly Gln Asn Val Val Gly Ile Gln Val Thr Glu Thr Ala
                325                 330                 335

Lys Val Asn Ile Trp Glu Glu Lys Glu Asn Val Gly Ser Phe Thr Asn
            340                 345                 350

Gln Met Thr Pro Glu Lys His Leu Asn Ser Leu Gly Asn Leu Ala Lys
        355                 360                 365

Ser Leu Asp Ala Glu Gln Asp Thr Thr Asn Pro Lys Pro Phe Trp Asn
    370                 375                 380

Met Gly Glu Asn Ser Lys Gln Leu Pro Gly Pro Gln Lys Cys Ser Asp
385                 390                 395                 400

Pro Arg Leu Leu Gln Glu Ser Phe Trp Lys Asn Tyr Ser Gln Leu Phe
                405                 410                 415

Trp Gly Leu Pro Ser Leu His Ser Glu Ser Leu Val Ala Asn Ala Trp
            420                 425                 430

Val Thr Asp Arg Ser Tyr Thr Leu Gln Ser Pro Pro Phe Leu Phe Asn
        435                 440                 445

Glu Met Ser Asn Val Cys Pro Ile Gln Arg Glu Thr Thr Met Ser Pro
    450                 455                 460

Leu Leu Phe Gln Ala Gln Pro Leu Ser His Arg Gln Pro Phe Ile Ser
465                 470                 475                 480

Ser Thr Pro Gln Phe Leu Pro Thr Pro Met Ala Gln Ala Glu Ala Gln
                485                 490                 495

Ala His Leu Gln Ser Ser Phe Pro Val Leu Ser Pro Ala Phe Pro Ser
            500                 505                 510

Leu Ile Lys Asn Thr Gly Val Ala Cys Pro Ala Ser Gln Asn Lys Val
        515                 520                 525

Gln Ala Leu Ser Leu Pro Glu Thr Gln His Pro Glu Trp Pro Leu Leu
    530                 535                 540

Arg Lys Gln Leu Glu Gly Arg Leu Ala Leu Pro Ser Arg Val Gln Lys
```

545 550 555 560

Ser Gln Asp Val Phe Ser Val Ser Thr Pro Asn Leu Pro Gln Glu Ser
565 570 575

Leu Thr Ser Ile Leu Pro Glu Asn Phe Pro Val Ser Pro Glu Leu Arg
580 585 590

Arg Gln Leu Glu Gln His Ile Lys Lys Trp Ile Ile Gln His Trp Gly
595 600 605

Asn Leu Gly Arg Ile Gln Glu Ser Leu Asp Leu Met Gln Leu Arg Asp
610 615 620

Glu Ser Pro Gly Thr Ser Gln Ala Lys Gly Lys Pro Ser Pro Trp Gln
625 630 635 640

Ser Ser Thr Ser Thr Gly Glu Ser Ser Lys Glu Ala Gln Lys Val Lys
645 650 655

Phe Gln Leu Glu Arg Asp Leu Cys Pro His Leu Gly Gln Ile Leu Gly
660 665 670

Glu Thr Pro Gln Asn Leu Ser Arg Asp Met Lys Ser Phe Pro Arg Lys
675 680 685

Val Leu Gly Val Thr Ser Glu Glu Ser Glu Arg Asn Leu Arg Lys Pro
690 695 700

Leu Arg Ser Asp Ser Gly Ser Asp Leu Leu Arg Cys Thr Glu Arg Thr
705 710 715 720

His Ile Glu Asn Ile Leu Lys Ala His Met Gly Arg Asn Leu Gly Gln
725 730 735

Thr Asn Glu Gly Leu Ile Pro Val Arg Val Arg Arg Ser Trp Leu Ala
740 745 750

Val Asn Gln Ala Leu Pro Val Ser Asn Thr His Val Lys Thr Ser Asn
755 760 765

Leu Ala Ala Pro Lys Ser Gly Lys Ala Cys Val Asn Thr Ala Gln Val
770 775 780

Leu Ser Phe Leu Glu Pro Cys Thr Gln Gln Gly Leu Gly Ala His Ile
785 790 795 800

```
Val Arg Phe Trp Ala Lys His Arg Trp Gly Leu Pro Leu Arg Val Leu
                805                 810                 815

Lys Pro Ile Gln Cys Phe Lys Leu Glu Lys Val Ser Ser Leu Ser Leu
            820                 825                 830

Thr Gln Leu Ala Gly Pro Ser Ser Ala Thr Cys Glu Ser Gly Ala Gly
        835                 840                 845

Ser Glu Val Glu Val Asp Met Phe Leu Arg Lys Pro Pro Met Ala Ser
    850                 855                 860

Leu Arg Lys Gln Val Leu Thr Lys Ala Ser Asp His Met Pro Glu Ser
865                 870                 875                 880

Leu Leu Ala Ser Ser Pro Ala Trp Lys Gln Phe Gln Arg Ala Pro Arg
                885                 890                 895

Gly Ile Pro Ser Trp Asn Asp His Gly Pro Leu Lys Pro Pro Pro Ala
            900                 905                 910

Gly Gln Glu Gly Arg Trp Pro Ser Lys Pro Leu Thr Tyr Ser Leu Thr
        915                 920                 925

Gly Ser Thr Gln Gln Ser Arg Ser Leu Gly Ala Gln Ser Ser Lys Ala
    930                 935                 940

Gly Glu Thr Arg Glu Ala Val Pro Gln Cys Arg Val Pro Leu Glu Thr
945                 950                 955                 960

Cys Met Leu Ala Asn Leu Gln Ala Thr Ser Glu Asp Val His Gly Phe
                965                 970                 975

Glu Ala Pro Gly Thr Ser Lys Ser Ser Leu His Pro Arg Val Ser Val
            980                 985                 990

Ser Gln Asp Pro Arg Lys Leu Cys  Leu Met Glu Glu Val  Val Ser Glu
        995                 1000                1005

Phe Glu  Pro Gly Met Ala Thr  Lys Ser Glu Thr Gln  Pro Gln Val
    1010                1015                1020

Cys Ala  Ala Val Val Leu Leu  Pro Asp Gly Gln Ala  Ser Val Val
    1025                1030                1035

Pro His  Ala Ser Glu Asn Leu  Val Ser Gln Val Pro  Gln Gly His
    1040                1045                1050
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Leu Gln  Ser Met Pro Thr Gly  Asn Met Arg Ala Ser  Gln Glu Leu
    1055                 1060                 1065

His Asp  Leu Met Ala Ala Arg  Arg Ser Lys Leu Val  Gln Glu Glu
    1070                 1075                 1080

Pro Arg  Asn Pro Asn Cys Gln  Gly Ser Cys Lys Ser  Gln Arg Pro
    1085                 1090                 1095

Met Phe  Pro Pro Ile His Lys  Ser Glu Lys Ser Arg  Lys Pro Asn
    1100                 1105                 1110

Leu Glu  Lys His Glu Glu Arg  Leu Glu Gly Leu Arg  Thr Pro Gln
    1115                 1120                 1125

Leu Thr  Pro Val Arg Lys Thr  Glu Asp Thr His Gln  Asp Glu Gly
    1130                 1135                 1140

Val Gln  Leu Leu Pro Ser Lys  Lys Gln Pro Pro Ser  Val Ser His
    1145                 1150                 1155

Phe Gly  Glu Asn Ile Lys Gln  Phe Phe Gln Trp Ile  Phe Ser Lys
    1160                 1165                 1170

Lys Lys  Ser Lys Pro Ala Pro  Val Thr Ala Glu Ser  Gln Lys Thr
    1175                 1180                 1185

Val Lys  Asn Arg Ser Cys Val  Tyr Ser Ser Ser Ala  Glu Ala Gln
    1190                 1195                 1200

Gly Leu  Met Thr Ala Val Gly  Gln Met Leu Asp Lys  Lys Met Ser
    1205                 1210                 1215

Leu Cys  His Ala His His Ala  Ser Lys Val Asn Gln  His Lys Gln
    1220                 1225                 1230

Lys Phe  Gln Ala Pro Val Cys  Gly Phe Pro Cys Asn  His Arg His
    1235                 1240                 1245

Leu Phe  Tyr Ser Glu His Gly  Arg Ile Leu Ser Tyr  Ala Ala Ser
    1250                 1255                 1260

Ser Gln  Gln Ala Thr Leu Lys  Ser Gln Gly Cys Pro  Asn Arg Asp
    1265                 1270                 1275

Arg Gln  Ile Arg Asn Gln Gln  Pro Leu Lys Ser Val  Arg Cys Asn
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Asn Glu Gln Trp Gly Leu Arg His Pro Gln Ile Leu His Pro Lys
1295 1300 1305

Lys Ala Val Ser Pro Val Ser Pro Pro Gln His Trp Pro Lys Thr
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Ser Gly Ala Ser Ser His His His His Cys Pro Arg His Cys Leu
1325 1330 1335

Leu Trp Glu Gly Ile
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tggacttgtc aactctgcca gtgtacgtgc catttctctt ccactatgag aggaccgatt 180

gtattgcaca tttgtctggc tttctgtagc cttctgcttt tcagcgttgc cacacaatgt 240

ctggccttcc ccaaaataga aaggaggagg gagatagcac atgttcatgc ggaaaaaggg 300

cagtccgata agatgaacac cgatgaccta gaaaatagct ctgttacctc aaagcagact 360

ccccaactgg tggtctctga agatccaatg atgatgtcag cagtaccatc ggcaacatca 420

ttaaataaag cattctcgat taacaaagaa acccagcctg gacaagctgg gctcatgcaa 480

acagaacgcc ctggtgtttc cacacctact gagtcaggtg tcccctcagc tgaagaagta 540

tttggttcca gccagccaga gagaatatct cctgaaagtg gacttgccaa ggccatgtta 600

accattgcta tcactgcgac tccttctctg actgttgatg aaaaggagga actccttaca 660

agcactaact ttcagcccat tgtagaagag atcacagaaa ccacaaaagg ttttctgaag 720

tatatggata atcaatcatt tgcaactgaa agtcaggaag gagttggttt gggacattca 780

ccttcatcct atgtgaatac taaggaaatg ctaaccacca atccaaagac tgagaaattt 840

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Arg Arg Arg Glu Ile Ala His Val His Ala Glu Lys Gly Gln Ser Asp
35 40 45

Lys Met Asn Thr Asp Asp Leu Glu Asn Ser Ser Val Thr Ser Lys Gln
50 55 60

Thr Pro Gln Leu Val Val Ser Glu Asp Pro Met Met Met Ser Ala Val
65 70 75 80

Pro Ser Ala Thr Ser Leu Asn Lys Ala Phe Ser Ile Asn Lys Glu Thr
85 90 95

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Gln Pro Gly Gln Ala Gly Leu Met Gln Thr Glu Arg Pro Gly Val Ser
            100                 105                 110

Thr Pro Thr Glu Ser Gly Val Pro Ser Ala Glu Glu Val Phe Gly Ser
        115                 120                 125

Ser Gln Pro Glu Arg Ile Ser Pro Glu Ser Gly Leu Ala Lys Ala Met
    130                 135                 140

Leu Thr Ile Ala Ile Thr Ala Thr Pro Ser Leu Thr Val Asp Glu Lys
145                 150                 155                 160

Glu Glu Leu Leu Thr Ser Thr Asn Phe Gln Pro Ile Val Glu Glu Ile
                165                 170                 175

Thr Glu Thr Thr Lys Gly Phe Leu Lys Tyr Met Asp Asn Gln Ser Phe
            180                 185                 190

Ala Thr Glu Ser Gln Glu Gly Val Gly Leu Gly His Ser Pro Ser Ser
        195                 200                 205

Tyr Val Asn Thr Lys Glu Met Leu Thr Thr Asn Pro Lys Thr Glu Lys
    210                 215                 220

Phe Glu Ala Asp Thr Asp His Arg Thr Thr Ser Phe Pro Gly Ala Glu
225                 230                 235                 240

Ser Thr Ala Gly Ser Glu Pro Gly Ser Leu Thr Pro Asp Lys Glu Lys
                245                 250                 255

Pro Ser Gln Met Thr Ala Asp Asn Thr Gln Ala Ala Ala Thr Lys Gln
            260                 265                 270

Pro Leu Glu Thr Ser Glu Tyr Thr Leu Ser Val Glu Pro Glu Thr Asp
        275                 280                 285

Ser Leu Leu Gly Ala Pro Glu Val Thr Val Ser Val Ser Thr Ala Val
    290                 295                 300

Pro Ala Ala Ser Ala Leu Ser Asp Glu Trp Asp Asp Thr Lys Leu Glu
305                 310                 315                 320

Ser Val Ser Arg Ile Arg Thr Pro Lys Leu Gly Asp Asn Glu Glu Thr
                325                 330                 335

Gln Val Arg Thr Glu Met Ser Gln Thr Ala Gln Val Ser His Glu Gly
            340                 345                 350
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Met Glu Gly Gly Gln Pro Trp Thr Glu Ala Ala Gln Val Ala Leu Gly
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Leu Pro Glu Gly Glu Thr His Thr Gly Thr Ala Leu Leu Ile Ala His
    370                 375                 380

Gly Asn Glu Arg Ser Pro Ala Phe Thr Asp Gln Ser Ser Phe Thr Pro
385                 390                 395                 400

Thr Ser Leu Met Glu Asp Met Lys Val Ser Ile Val Asn Leu Leu Gln
                405                 410                 415

Ser Thr Gly Asp Phe Thr Glu Ser Thr Lys Glu Asn Asp Ala Leu Phe
            420                 425                 430

Phe Leu Glu Thr Thr Val Ser Val Ser Val Tyr Glu Ser Glu Ala Asp
        435                 440                 445

Gln Leu Leu Gly Asn Thr Met Lys Asp Ile Ile Thr Gln Glu Met Thr
    450                 455                 460

Thr Ala Val Gln Glu Pro Asp Ala Thr Leu Ser Met Val Thr Gln Glu
465                 470                 475                 480

Gln Val Ala Thr Leu Glu Leu Ile Arg Asp Ser Gly Lys Thr Glu Glu
                485                 490                 495

Glu Lys Glu Asp Pro Ser Pro Val Ser Asp Val Pro Gly Val Thr Gln
            500                 505                 510

Leu Ser Arg Arg Trp Glu Pro Leu Ala Thr Thr Ile Ser Thr Thr Val
        515                 520                 525

Val Pro Leu Ser Phe Glu Val Thr Pro Thr Val Glu Glu Gln Met Asp
    530                 535                 540

Thr Val Thr Gly Pro Asn Glu Glu Phe Thr Pro Val Leu Gly Ser Pro
545                 550                 555                 560

Val Thr Pro Pro Gly Ile Met Val Gly Glu Pro Ser Ile Ser Pro Ala
                565                 570                 575

Leu Pro Ala Leu Glu Ala Ser Ser Glu Arg Arg Thr Val Val Pro Ser
            580                 585                 590

Ile Thr Arg Val Asn Thr Ala Ala Ser Tyr Gly Leu Asp Gln Leu Glu
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595 600 605

Ser Glu Glu Gly Gln Glu Asp Glu Asp Glu Glu Asp Glu Glu Asp Glu
610 615 620

Asp Glu Glu Glu Glu Asp Glu Glu Glu Asp Glu Glu Asp Lys Asp Ala
625 630 635 640

Asp Ser Leu Asp Glu Gly Leu Asp Gly Asp Thr Glu Leu Pro Gly Phe
645 650 655

Thr Leu Pro Gly Ile Thr Ser Gln Glu Pro Gly Leu Glu Glu Gly Asn
660 665 670

Met Asp Leu Leu Glu Gly Ala Thr Tyr Gln Val Pro Asp Ala Leu Glu
675 680 685

Trp Glu Gln Gln Asn Gln Gly Leu Val Arg Ser Trp Met Glu Lys Leu
690 695 700

Lys Asp Lys Ala Gly Tyr Met Ser Gly Met Leu Val Pro Val Gly Val
705 710 715 720

Gly Ile Ala Gly Ala Leu Phe Ile Leu Gly Ala Leu Tyr Ser Ile Lys
725 730 735

Val Met Asn Arg Arg Arg Arg Asn Gly Phe Lys Arg His Lys Arg Lys
740 745 750

Gln Arg Glu Phe Asn Ser Met Gln Asp Arg Val Met Leu Leu Ala Asp
755 760 765

Ser Ser Glu Asp Glu Phe
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<400> 130

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Arg Glu Lys Gln Lys Arg Asn Met Glu Glu Leu Lys Lys Glu Val Val
35 40 45

Met Asp Asp His Lys Leu Thr Leu Glu Glu Leu Ser Thr Lys Tyr Ser
50 55 60

Val Asp Leu Thr Lys Gly His Ser His Gln Arg Ala Lys Glu Ile Leu
65 70 75 80

Thr Arg Gly Gly Pro Asn Thr Val Thr Pro Pro Pro Thr Thr Pro Glu
85 90 95

Trp Val Lys Phe Cys Lys Gln Leu Phe Gly Gly Phe Ser Leu Leu Leu
100 105 110

Trp Thr Gly Ala Ile Leu Cys Phe Val Ala Tyr Ser Ile Gln Ile Tyr
115 120 125

Phe Asn Glu Glu Pro Thr Lys Asp Asn Leu Tyr Leu Ser Ile Val Leu
130 135 140

Ser Val Val Val Ile Val Thr Gly Cys Phe Ser Tyr Tyr Gln Glu Ala
145 150 155 160

Lys Ser Ser Lys Ile Met Glu Ser Phe Lys Asn Met Val Pro Gln Gln
165 170 175

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Ala Leu Val Ile Arg Gly Gly Glu Lys Met Gln Ile Asn Val Gln Glu
            180                 185                 190

Val Val Leu Gly Asp Leu Val Glu Ile Lys Gly Gly Asp Arg Val Pro
        195                 200                 205

Ala Asp Leu Arg Leu Ile Ser Ala Gln Gly Cys Lys Val Asp Asn Ser
    210                 215                 220

Ser Leu Thr Gly Glu Ser Glu Pro Gln Ser Arg Ser Pro Asp Phe Thr
225                 230                 235                 240

His Glu Asn Pro Leu Glu Thr Arg Asn Ile Cys Phe Phe Ser Thr Asn
                245                 250                 255

Cys Val Glu Gly Thr Ala Arg Gly Ile Val Ile Ala Thr Gly Asp Ser
            260                 265                 270

Thr Val Met Gly Arg Ile Ala Ser Leu Thr Ser Gly Leu Ala Val Gly
        275                 280                 285

Gln Thr Pro Ile Ala Ala Glu Ile Glu His Phe Ile His Leu Ile Thr
    290                 295                 300

Val Val Ala Val Phe Leu Gly Val Thr Phe Phe Ala Leu Ser Leu Leu
305                 310                 315                 320

Leu Gly Tyr Gly Trp Leu Glu Ala Ile Ile Phe Leu Ile Gly Ile Ile
                325                 330                 335

Val Ala Asn Val Pro Glu Gly Leu Leu Ala Thr Val Thr Val Cys Leu
            340                 345                 350

Thr Leu Thr Ala Lys Arg Met Ala Arg Lys Asn Cys Leu Val Lys Asn
        355                 360                 365

Leu Glu Ala Val Glu Thr Leu Gly Ser Thr Ser Thr Ile Cys Ser Asp
    370                 375                 380

Lys Thr Gly Thr Leu Thr Gln Asn Arg Met Thr Val Ala His Met Trp
385                 390                 395                 400

Phe Asp Met Thr Val Tyr Glu Ala Asp Thr Thr Glu Glu Gln Thr Gly
                405                 410                 415

Lys Thr Phe Thr Lys Ser Ser Asp Thr Trp Phe Met Leu Ala Arg Ile
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Ala Gly Leu Cys Asn Arg Ala Asp Phe Lys Ala Asn Gln Glu Ile Leu
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Pro Ile Ala Lys Arg Ala Thr Thr Gly Asp Ala Ser Glu Ser Ala Leu
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Leu Lys Phe Ile Glu Gln Ser Tyr Ser Ser Val Ala Glu Met Arg Glu
465 470 475 480

Lys Asn Pro Lys Val Ala Glu Ile Pro Phe Asn Ser Thr Asn Lys Tyr
485 490 495

Gln Met Ser Ile His Leu Arg Glu Asp Ser Ser Gln Thr His Val Leu
500 505 510

Met Met Lys Gly Ala Pro Glu Arg Ile Leu Glu Phe Cys Ser Thr Phe
515 520 525

Leu Leu Asn Gly Gln Glu Tyr Ser Met Asn Asp Glu Met Lys Glu Ala
530 535 540

Phe Gln Asn Ala Tyr Leu Glu Leu Gly Gly Leu Gly Glu Arg Val Leu
545 550 555 560

Gly Phe Cys Phe Leu Asn Leu Pro Ser Ser Phe Ser Lys Gly Phe Pro
565 570 575

Phe Asn Thr Asp Glu Ile Asn Phe Pro Met Asp Asn Leu Cys Phe Val
580 585 590

Gly Leu Ile Ser Met Ile Asp Pro Pro Arg Ala Ala Val Pro Asp Ala
595 600 605

Val Ser Lys Cys Arg Ser Ala Gly Ile Lys Val Ile Met Val Thr Gly
610 615 620

Asp His Pro Ile Thr Ala Lys Ala Ile Ala Lys Gly Val Gly Ile Ile
625 630 635 640

Ser Glu Gly Thr Glu Thr Ala Glu Glu Val Ala Ala Arg Leu Lys Ile
645 650 655

Pro Ile Ser Lys Val Asp Ala Ser Ala Ala Lys Ala Ile Val Val His
660 665 670

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Gly Ala Glu Leu Lys Asp Ile Gln Ser Lys Gln Leu Asp Gln Ile Leu
        675                 680                 685

Gln Asn His Pro Glu Ile Val Phe Ala Arg Thr Ser Pro Gln Gln Lys
    690                 695                 700

Leu Ile Ile Val Glu Gly Cys Gln Arg Leu Gly Ala Val Val Ala Val
705                 710                 715                 720

Thr Gly Asp Gly Val Asn Asp Ser Pro Ala Leu Lys Lys Ala Asp Ile
                725                 730                 735

Gly Ile Ala Met Gly Ile Ser Gly Ser Asp Val Ser Lys Gln Ala Ala
            740                 745                 750

Asp Met Ile Leu Leu Asp Asp Asn Phe Ala Ser Ile Val Thr Gly Val
        755                 760                 765

Glu Glu Gly Arg Leu Ile Phe Asp Asn Leu Lys Lys Ser Ile Met Tyr
    770                 775                 780

Thr Leu Thr Ser Asn Ile Pro Glu Ile Thr Pro Phe Leu Met Phe Ile
785                 790                 795                 800

Ile Leu Gly Ile Pro Leu Pro Leu Gly Thr Ile Thr Ile Leu Cys Ile
                805                 810                 815

Asp Leu Gly Thr Asp Met Val Pro Ala Ile Ser Leu Ala Tyr Glu Ser
            820                 825                 830

Ala Glu Ser Asp Ile Met Lys Arg Leu Pro Arg Asn Pro Lys Thr Asp
        835                 840                 845

Asn Leu Val Asn His Arg Leu Ile Gly Met Ala Tyr Gly Gln Ile Gly
    850                 855                 860

Met Ile Gln Ala Leu Ala Gly Phe Phe Thr Tyr Phe Val Ile Leu Ala
865                 870                 875                 880

Glu Asn Gly Phe Arg Pro Val Asp Leu Leu Gly Ile Arg Leu His Trp
                885                 890                 895

Glu Asp Lys Tyr Leu Asn Asp Leu Glu Asp Ser Tyr Gly Gln Gln Trp
            900                 905                 910

Thr Tyr Glu Gln Arg Lys Val Val Glu Phe Thr Cys Gln Thr Ala Phe
        915                 920                 925
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Phe Val Thr Ile Val Val Val Gln Trp Ala Asp Leu Ile Ile Ser Lys
930 935 940

Thr Arg Arg Asn Ser Leu Phe Gln Gln Gly Met Arg Asn Lys Val Leu
945 950 955 960

Ile Phe Gly Ile Leu Glu Glu Thr Leu Leu Ala Ala Phe Leu Ser Tyr
965 970 975

Thr Pro Gly Met Asp Val Ala Leu Arg Met Tyr Pro Leu Lys Ile Thr
980 985 990

Trp Trp Leu Cys Ala Ile Pro Tyr Ser Ile Leu Ile Phe Val Tyr Asp
995 1000 1005

Glu Ile Arg Lys Leu Leu Ile Arg Gln His Pro Asp Gly Trp Val
1010 1015 1020

Glu Arg Glu Thr Tyr Tyr
1025

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<211> 21
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<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 131
tgtaatcctg gctgagaatg g 21

<210> 132
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 132
aagtgagttg cggcgagt 18

<210> 133
<211> 279
<212> DNA
<213> Homo sapiens

<400> 133
atgtatgtaa aaattgcaaa acatctcaat gatgtttatg ccccccagaa ggtactgtgt 60

cacgggatct catatattct ggctgtcatt gtcataataa gccactcttg gtcatatgga 120

aaagcattca gctgctccct gcctttgctc acagcgtgtg gtactctctt agaagctatt 180

cctgtcctat ttaggcagtt attcctgctt cttgtgttgg acctgaagtc aacagggcca 240

gcaatagaga agaaagatga tgtgaaggag agcaactga 279

<210> 134
<211> 92
<212> PRT
<213> Homo sapiens

<400> 134

Met Tyr Val Lys Ile Ala Lys His Leu Asn Asp Val Tyr Ala Pro Gln
1 5 10 15

Lys Val Leu Cys His Gly Ile Ser Tyr Ile Leu Ala Val Ile Val Ile
20 25 30

Ile Ser His Ser Trp Ser Tyr Gly Lys Ala Phe Ser Cys Ser Leu Pro
35 40 45

Leu Leu Thr Ala Cys Gly Thr Leu Leu Glu Ala Ile Pro Val Leu Phe
50 55 60

Arg Gln Leu Phe Leu Leu Leu Val Leu Asp Leu Lys Ser Thr Gly Pro
65 70 75 80

Ala Ile Glu Lys Lys Asp Asp Val Lys Glu Ser Asn
85 90

<210> 135
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 135
tgctccctgc ctttgctcac 20

<210> 136
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 136
ggtacttggt ctcgaacgat gatc 24

<210> 137
<211> 1569
<212> DNA
<213> Homo sapiens

<400> 137
atgcctgtag ggggtggccc tgagagtgtg ggcaggtgca atggctgtca atgccacata 60

aagggcaagg ggatctacat cctaaacagt gaaagaccag tgcccggaga ctacatctac 120

atcaggaaga agaagcagca aaattctgac ccacagccca agaggggtcg gggcagcaga 180

acctcagcca cagccaatca cagcggggtc cttcggggag gggcgtggcc tgacaacttc 240

ggcgacgcgg ctggaccaat ccggacggag gagagcgaag ctcctctgca ctgggcccag 300

gtgcgctcct cagcgtctcc gggtggcggg gcgcgcggga tggaggagtc ttgggaggct 360

gcgcccggag gccaagccgg ggcagagctc ccaatggagc ccgtgggaag cctggtcccc 420

acgctggagc agccgcaggt gcccgcgaag gtgcgacaac ctgaaggtcc cgaaagcagc 480

ccaagtccgg ccggggccgt ggagaaggcg gcgggcgcag gcctggagcc ctcgagcaag 540

aaaaagccgc cttcgcctcg ccccgggtcc ccgcgcgtgc cgccgctcag cctgggctac 600

ggggtctgcc ccgagccgcc gtcaccgggc cctgccttgg tcaagctgcc ccggaatggc 660

gaggcgcccg gggctgagcc tgcgcccagc gcctgggcgc ccatggagct gcaggtagat 720

gtgcgcgtga agcccgtggg cgcggccggt ggcagcagca cgccatcgcc caggccctcc 780

acgcgcttcc tcaaggtgcc ggtgcccgag tcccctgcct tctcccgcca cgcggacccg 840

gcgcaccagc tcctgctgcg cgcaccatcc cagggcggca cgtggggccg ccgctcgccg 900

ctggctgcag cccggacgga gagcggctgc gacgcagagg gccgggccag ccccgcggaa 960

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gccgtaacgc ttacggggct acccatgtac gtgaagtccc tgtactgggc cctggcgttc 1140

atggctgtgc tcctggcagt ctctggggtt gtcattgtgg tcctggcctc aagagcagga 1200

gccagatgcc agcagtgccc cccaggctgg gtgttgtccg aggagcactg ttactacttc 1260

tctgcagaag cgcaggcctg ggaagccagc caggctttct gctcagccta ccacgctacc 1320

ctccccctgc taagccacac ccaggacttc ctgggcagat acccagtctc caggcactcc 1380

tgggtggggg cctggcgagg cccccagggc tggcactgga tcgacgaggc cccactcccg 1440

ccccagctac tccctgagga cggcgaggac aatctggata tcaactgtgg ggccctggag 1500

gaaggcacgc tggtggctgc aaactgcagc actccaagac cctgggtctg tgccaagggg 1560

acccagtga 1569

<210> 138

<211> 522
<212> PRT
<213> Homo sapiens

<400> 138

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Met Pro Val Gly Gly Gly Pro Glu Ser Val Gly Arg Cys Asn Gly Cys
1               5                  10                  15

Gln Cys His Ile Lys Gly Lys Gly Ile Tyr Ile Leu Asn Ser Glu Arg
            20                  25                  30

Pro Val Pro Gly Asp Tyr Ile Tyr Ile Arg Lys Lys Lys Gln Gln Asn
        35                  40                  45

Ser Asp Pro Gln Pro Lys Arg Gly Arg Gly Ser Arg Thr Ser Ala Thr
    50                  55                  60

Ala Asn His Ser Gly Val Leu Arg Gly Gly Ala Trp Pro Asp Asn Phe
65                  70                  75                  80

Gly Asp Ala Ala Gly Pro Ile Arg Thr Glu Glu Ser Glu Ala Pro Leu
                85                  90                  95

His Trp Ala Gln Val Arg Ser Ser Ala Ser Pro Gly Gly Gly Ala Arg
            100                 105                 110

Gly Met Glu Glu Ser Trp Glu Ala Ala Pro Gly Gly Gln Ala Gly Ala
        115                 120                 125

Glu Leu Pro Met Glu Pro Val Gly Ser Leu Val Pro Thr Leu Glu Gln
    130                 135                 140

Pro Gln Val Pro Ala Lys Val Arg Gln Pro Glu Gly Pro Glu Ser Ser
145                 150                 155                 160

Pro Ser Pro Ala Gly Ala Val Glu Lys Ala Ala Gly Ala Gly Leu Glu
                165                 170                 175

Pro Ser Ser Lys Lys Lys Pro Pro Ser Pro Arg Pro Gly Ser Pro Arg
            180                 185                 190

Val Pro Pro Leu Ser Leu Gly Tyr Gly Val Cys Pro Glu Pro Pro Ser
        195                 200                 205

Pro Gly Pro Ala Leu Val Lys Leu Pro Arg Asn Gly Glu Ala Pro Gly
    210                 215                 220
```

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Ala Glu Pro Ala Pro Ser Ala Trp Ala Pro Met Glu Leu Gln Val Asp
225                 230                 235                 240

Val Arg Val Lys Pro Val Gly Ala Ala Gly Gly Ser Ser Thr Pro Ser
                245                 250                 255

Pro Arg Pro Ser Thr Arg Phe Leu Lys Val Pro Val Pro Glu Ser Pro
            260                 265                 270

Ala Phe Ser Arg His Ala Asp Pro Ala His Gln Leu Leu Leu Arg Ala
        275                 280                 285

Pro Ser Gln Gly Gly Thr Trp Gly Arg Arg Ser Pro Leu Ala Ala Ala
    290                 295                 300

Arg Thr Glu Ser Gly Cys Asp Ala Glu Gly Arg Ala Ser Pro Ala Glu
305                 310                 315                 320

Gly Ser Ala Gly Ser Pro Gly Ser Pro Thr Cys Cys Arg Cys Lys Glu
                325                 330                 335

Leu Gly Leu Glu Lys Glu Asp Ala Ala Leu Leu Pro Arg Ala Gly Leu
            340                 345                 350

Asp Gly Asp Glu Lys Leu Pro Arg Ala Val Thr Leu Thr Gly Leu Pro
        355                 360                 365

Met Tyr Val Lys Ser Leu Tyr Trp Ala Leu Ala Phe Met Ala Val Leu
    370                 375                 380

Leu Ala Val Ser Gly Val Val Ile Val Val Leu Ala Ser Arg Ala Gly
385                 390                 395                 400

Ala Arg Cys Gln Gln Cys Pro Pro Gly Trp Val Leu Ser Glu Glu His
                405                 410                 415

Cys Tyr Tyr Phe Ser Ala Glu Ala Gln Ala Trp Glu Ala Ser Gln Ala
            420                 425                 430

Phe Cys Ser Ala Tyr His Ala Thr Leu Pro Leu Leu Ser His Thr Gln
        435                 440                 445

Asp Phe Leu Gly Arg Tyr Pro Val Ser Arg His Ser Trp Val Gly Ala
    450                 455                 460

Trp Arg Gly Pro Gln Gly Trp His Trp Ile Asp Glu Ala Pro Leu Pro
465                 470                 475                 480
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Pro Gln Leu Leu Pro Glu Asp Gly Glu Asp Asn Leu Asp Ile Asn Cys
485 490 495

Gly Ala Leu Glu Glu Gly Thr Leu Val Ala Ala Asn Cys Ser Thr Pro
500 505 510

Arg Pro Trp Val Cys Ala Lys Gly Thr Gln
515 520

<210> 139
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 139
gagaaggagg atgcggcg 18

<210> 140
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 140
ggaccacaat gacaacccca g 21

<210> 141
<211> 2217
<212> DNA
<213> Homo sapiens

<400> 141
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ttccagactt atcgggccca taaaataaaa gccaaaagaa gcatagccac tcctgaaaac 120

ctgaagaaat tattgccacg tgttcccaaa aacagtgccc tgagtgatga aatgacaaag 180

cttcacaaag gagctaagcc atgcaaatca aatacatttg gatgttttcc tattcatcag 240

gctgtacttt caggttccaa agaatgcatg gaaataatat tgaagtttgg tgaagagcac 300

gggtacagca gacagtgtca catcaacttt gtggataacg ggaaagccag ccctctccat 360

ctggctgtgc aaaatggtga cttggaaatg atgaaaatgt gcctggacaa tggtgtacaa 420

atagacctag tggagatgca acagatcaaa gagctggtaa tggatgaaga caacgatggg 480

tgtactcctc tacattatgc atgtagacag gggggccctg gttctgtaaa taacctactt 540

ggctttaatg tgtccattca ttccaaaagc aaagataaga aatcacctct gcattttgca 600

gccagttatg ggcgtatcaa tacctgtcag aggctcctac aagacataag tgatacgagg 660

cttctgaatg aaggggacct tcatggaatg actcctctcc atctggcagc aaagaatgga 720

catgataaag tagttcagct tcttctgaaa aaaggtgcat tgtttctcag atgggatgaa 780

tgtcttaagg tttttagtca ttattctcca aacaataaat gtccaatttt ggaaatgatc 840

gaatacctcc ctgaatgcat gaagaaagtt ctacccttct tttctaatgt tcacgtaaga 900

cctgctccaa accagaatca aataaaccat ggagaacaca ggttggctta cggatttata 960

gcccatatga taaatctagg attttactgt cttggtctca taccaatgac ctttcttgtt 1020

gtcagaataa aaccaggaat ggctttcaac tctgctggaa tcatcaataa aactagtgat 1080

cattcagaaa tactagataa catgaattca agtctaataa caatttgtat gattttagtt 1140

ttttgctcaa gtatattagg gtatgtcaaa gaagtggttc aaattttcca acagaaaagg 1200

aattacttta tggatattag cagtagtact gaatggatta tcaacacgat gggccccatt 1260

ttagtgctgc ccttgttcac tgaaatagca gcccatctgc aatttgagaa ttgtggaatt 1320

ttcattgtta tattggaggt aatttttaaa actttgttga ggtctgcagt tgtatttttc 1380

ttccttcttt tggcttttgg actcagcttt tacgtcctcc tgaatttaca gtccttccta 1440

gaaccatttc tgaagaataa attggcacat ccagttctgt cctttgcaca gcttatttcc 1500

ttcacagtat ttgccccaat tgtcctcatg aatttactta ttggtttggc agttggtgac 1560

attgctgagg tccagaaaca tgcatcattg aagaggatag ctatgcagaa gctgccatgc 1620

tgttgcatac gcaaagtgga tcggaaatcc accgccgtat gtcccaacaa acccagatgt 1680

gatgggacat tatttcaagt cctactcgct ctaggccccc tacccctaga agaaaataga 1740

aacataaaaa gttttcttcc tactgagatc actgttaaga ggactcacga acaccttcct 1800

tctgcaggtt ttggtcatca tgggaaacat accttgtcct tgcttttggt agaagagtgg 1860

cttcctctga atgtagtaca ctcctcttgc tctgccttca gagtggttgg ccagatcttt 1920

cccattagac attttcagtg gattcatgtg aatgagccgc acactggcaa tttaaaagag 1980

aaattggctg ctccatacat cactcaccag atcaagccat tcttgcgagc agctggtttt 2040

tgcacagtga aggtggtcca gagagatgac atctctgtgt ggagtgtgga tttcaggtgg 2100

ctcaatgcat gggaagcagc gattcgaaag cagtctctca gacaatctga gatggaggaa 2160

ctgagctgct cgctgctgct gcgtgtcact gatgtgcaca caagaagctt gtattag 2217

<210> 142
<211> 738
<212> PRT
<213> Homo sapiens

<400> 142

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Met Val Cys Thr Phe Asp Ser Glu Leu Leu Asn Cys Gln Arg Lys Asp
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Glu Tyr Asn Gln Phe Gln Thr Tyr Arg Ala His Lys Ile Lys Ala Lys
            20                  25                  30

Arg Ser Ile Ala Thr Pro Glu Asn Leu Lys Lys Leu Leu Pro Arg Val
        35                  40                  45

Pro Lys Asn Ser Ala Leu Ser Asp Glu Met Thr Lys Leu His Lys Gly
    50                  55                  60

Ala Lys Pro Cys Lys Ser Asn Thr Phe Gly Cys Phe Pro Ile His Gln
65                  70                  75                  80

Ala Val Leu Ser Gly Ser Lys Glu Cys Met Glu Ile Ile Leu Lys Phe
                85                  90                  95

Gly Glu Glu His Gly Tyr Ser Arg Gln Cys His Ile Asn Phe Val Asp
            100                 105                 110

Asn Gly Lys Ala Ser Pro Leu His Leu Ala Val Gln Asn Gly Asp Leu
        115                 120                 125

Glu Met Met Lys Met Cys Leu Asp Asn Gly Val Gln Ile Asp Leu Val
    130                 135                 140

Glu Met Gln Gln Ile Lys Glu Leu Val Met Asp Glu Asp Asn Asp Gly
145                 150                 155                 160

Cys Thr Pro Leu His Tyr Ala Cys Arg Gln Gly Gly Pro Gly Ser Val
                165                 170                 175

Asn Asn Leu Leu Gly Phe Asn Val Ser Ile His Ser Lys Ser Lys Asp
            180                 185                 190

Lys Lys Ser Pro Leu His Phe Ala Ala Ser Tyr Gly Arg Ile Asn Thr
        195                 200                 205

Cys Gln Arg Leu Leu Gln Asp Ile Ser Asp Thr Arg Leu Leu Asn Glu
    210                 215                 220

Gly Asp Leu His Gly Met Thr Pro Leu His Leu Ala Ala Lys Asn Gly
225                 230                 235                 240

His Asp Lys Val Val Gln Leu Leu Leu Lys Lys Gly Ala Leu Phe Leu
                245                 250                 255
```

```
Arg Trp Asp Glu Cys Leu Lys Val Phe Ser His Tyr Ser Pro Asn Asn
            260                 265                 270

Lys Cys Pro Ile Leu Glu Met Ile Glu Tyr Leu Pro Glu Cys Met Lys
        275                 280                 285

Lys Val Leu Pro Phe Phe Ser Asn Val His Val Arg Pro Ala Pro Asn
    290                 295                 300

Gln Asn Gln Ile Asn His Gly Glu His Arg Leu Ala Tyr Gly Phe Ile
305                 310                 315                 320

Ala His Met Ile Asn Leu Gly Phe Tyr Cys Leu Gly Leu Ile Pro Met
                325                 330                 335

Thr Phe Leu Val Val Arg Ile Lys Pro Gly Met Ala Phe Asn Ser Ala
            340                 345                 350

Gly Ile Ile Asn Lys Thr Ser Asp His Ser Glu Ile Leu Asp Asn Met
        355                 360                 365

Asn Ser Ser Leu Ile Thr Ile Cys Met Ile Leu Val Phe Cys Ser Ser
    370                 375                 380

Ile Leu Gly Tyr Val Lys Glu Val Val Gln Ile Phe Gln Gln Lys Arg
385                 390                 395                 400

Asn Tyr Phe Met Asp Ile Ser Ser Ser Thr Glu Trp Ile Ile Asn Thr
                405                 410                 415

Met Gly Pro Ile Leu Val Leu Pro Leu Phe Thr Glu Ile Ala Ala His
            420                 425                 430

Leu Gln Phe Glu Asn Cys Gly Ile Phe Ile Val Ile Leu Glu Val Ile
        435                 440                 445

Phe Lys Thr Leu Leu Arg Ser Ala Val Val Phe Phe Phe Leu Leu Leu
    450                 455                 460

Ala Phe Gly Leu Ser Phe Tyr Val Leu Leu Asn Leu Gln Ser Phe Leu
465                 470                 475                 480

Glu Pro Phe Leu Lys Asn Lys Leu Ala His Pro Val Leu Ser Phe Ala
                485                 490                 495

Gln Leu Ile Ser Phe Thr Val Phe Ala Pro Ile Val Leu Met Asn Leu
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500 505 510

Leu Ile Gly Leu Ala Val Gly Asp Ile Ala Glu Val Gln Lys His Ala
515 520 525

Ser Leu Lys Arg Ile Ala Met Gln Lys Leu Pro Cys Cys Cys Ile Arg
530 535 540

Lys Val Asp Arg Lys Ser Thr Ala Val Cys Pro Asn Lys Pro Arg Cys
545 550 555 560

Asp Gly Thr Leu Phe Gln Val Leu Leu Ala Leu Gly Pro Leu Pro Leu
565 570 575

Glu Glu Asn Arg Asn Ile Lys Ser Phe Leu Pro Thr Glu Ile Thr Val
580 585 590

Lys Arg Thr His Glu His Leu Pro Ser Ala Gly Phe Gly His His Gly
595 600 605

Lys His Thr Leu Ser Leu Leu Leu Val Glu Glu Trp Leu Pro Leu Asn
610 615 620

Val Val His Ser Ser Cys Ser Ala Phe Arg Val Val Gly Gln Ile Phe
625 630 635 640

Pro Ile Arg His Phe Gln Trp Ile His Val Asn Glu Pro His Thr Gly
645 650 655

Asn Leu Lys Glu Lys Leu Ala Ala Pro Tyr Ile Thr His Gln Ile Lys
660 665 670

Pro Phe Leu Arg Ala Ala Gly Phe Cys Thr Val Lys Val Val Gln Arg
675 680 685

Asp Asp Ile Ser Val Trp Ser Val Asp Phe Arg Trp Leu Asn Ala Trp
690 695 700

Glu Ala Ala Ile Arg Lys Gln Ser Leu Arg Gln Ser Glu Met Glu Glu
705 710 715 720

Leu Ser Cys Ser Leu Leu Leu Arg Val Thr Asp Val His Thr Arg Ser
725 730 735

Leu Tyr

<210> 143
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 143
ttccttactc tccgctttcc 20

<210> 144
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 144
aactttgtgg ataacgggaa 20

<210> 145
<211> 1155
<212> DNA
<213> Homo sapiens

<400> 145
atgcagtctc tcatctcgcc ggtgaccaag gcgatcctgg tggccctctt catcttcgcc 60

atcctcctca tcctctacgt gatcctctgg gacgcaccgg ggagagcggg tgagtgcgct 120

cgtgcgggcg ctttgggggg ccacggttgg ggagccccaa cttcggggag gacgcggaat 180

ccggacgcgg gactgaaccc gaggattcac ggagcccggg gctcccctat ggggcacggg 240

aagcggcaga tgcgcgtgca gagaggtccg tcccacccac cccctgggcg ccttgggtcc 300

aaggcgcata ggcgctcccg cctgtggccg ccaccggtgc agcagaacgc gggctctcgg 360

gtgggtccaa tgcgctatgg cacaccaggc gctatcgggt ccctagccct ctgctccggc 420

ggtggggacc ccgcactcaa gttccctata acctccatgg acaaacacgg aaaaatcatg 480

tcttggaaga acagcatcgc cctacagata cagactaggc actttgcaca tgaaacaaga 540

gtcccagaaa tttctagaag caaatctcgc attcgtgacc gccagaccta cgggatgtac 600

cactttggga attttggaga agaaagaata aaggcagaaa tgaggataca gaaagcatgt 660

cacttgaaga tcaagaagtc aagcttggat gccaatggta aagtggatga tggtgaggat 720

gatgatggtg aggatgatga tggtgaggat gatgatggtg atgatgatgg tgaggatgat 780

gatggtgagg atgatgatgg tgaggatgat gatggtgagg atgatggtga ggatgatgat 840

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atgaagaatg ttgttggtaa ttacagactt cctgagctac caacttggac atctgtacaa 1140

cgatacaaat tttga 1155

<210> 146
<211> 384
<212> PRT
<213> Homo sapiens

<400> 146

Met Gln Ser Leu Ile Ser Pro Val Thr Lys Ala Ile Leu Val Ala Leu
1 5 10 15

Phe Ile Phe Ala Ile Leu Leu Ile Leu Tyr Val Ile Leu Trp Asp Ala
20 25 30

Pro Gly Arg Ala Gly Glu Cys Ala Arg Ala Gly Ala Leu Gly Gly His
35 40 45

Gly Trp Gly Ala Pro Thr Ser Gly Arg Thr Arg Asn Pro Asp Ala Gly
50 55 60

Leu Asn Pro Arg Ile His Gly Ala Arg Gly Ser Pro Met Gly His Gly
65 70 75 80

Lys Arg Gln Met Arg Val Gln Arg Gly Pro Ser His Pro Pro Pro Gly
85 90 95

Arg Leu Gly Ser Lys Ala His Arg Arg Ser Arg Leu Trp Pro Pro Pro
100 105 110

Val Gln Gln Asn Ala Gly Ser Arg Val Gly Pro Met Arg Tyr Gly Thr
115 120 125

Pro Gly Ala Ile Gly Ser Leu Ala Leu Cys Ser Gly Gly Gly Asp Pro
130 135 140

Ala Leu Lys Phe Pro Ile Thr Ser Met Asp Lys His Gly Lys Ile Met
145 150 155 160

Ser Trp Lys Asn Ser Ile Ala Leu Gln Ile Gln Thr Arg His Phe Ala
165 170 175

His Glu Thr Arg Val Pro Glu Ile Ser Arg Ser Lys Ser Arg Ile Arg
180 185 190

```
Asp Arg Gln Thr Tyr Gly Met Tyr His Phe Gly Asn Phe Gly Glu Glu
        195                 200                 205

Arg Ile Lys Ala Glu Met Arg Ile Gln Lys Ala Cys His Leu Lys Ile
    210                 215                 220

Lys Lys Ser Ser Leu Asp Ala Asn Gly Lys Val Asp Asp Gly Glu Asp
225                 230                 235                 240

Asp Asp Gly Glu Asp Asp Asp Gly Glu Asp Asp Asp Gly Asp Asp Asp
                245                 250                 255

Gly Glu Asp Asp Asp Gly Glu Asp Asp Asp Gly Glu Asp Asp Asp Gly
            260                 265                 270

Glu Asp Asp Gly Glu Asp Asp Asp Gly Asp Asp Asp Gly Glu Asp Asp
        275                 280                 285

Asp Gly Asp Asp Asp Gly Asp Asp Asp Gly Glu Asp Asp Asp Gly Glu
    290                 295                 300

Asp Asp Asp Gly Asp Ser Glu Asp Asp Gly Glu Asp Gly Asp Asp Asp
305                 310                 315                 320

Gly Glu Asp Asp Asp Gly Asp Ser Glu Asp Asp Gly Asp Asp Gly Asp
                325                 330                 335

Asp Asp Gly Glu Asp Asp Asp His Gly Asp Asp Val Arg Met Met Met
            340                 345                 350

Met Met Val Met Thr Val Thr Met Met Lys Asn Val Val Gly Asn Tyr
        355                 360                 365

Arg Leu Pro Glu Leu Pro Thr Trp Thr Ser Val Gln Arg Tyr Lys Phe
    370                 375                 380
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<210> 147
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 147
tccatgctgc cagcttcata c 21

<210> 148

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 148
ctcacaagtg atgagattga g 21

<210> 149
<211> 4384
<212> DNA
<213> Homo sapiens

<400> 149
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actttaaagc agcttaatct ttaaggaaca tatctctgat ctgggtaatt tgtagaactt 120

aatttgaggg tcattacatg tgaggatagc aggagttgaa gatgccaagg acctgaaggg 180

ctactggagg gacaggtgaa gtgatttgaa gatgtagcat tttgaatctc tttctggccc 240

atcctctgct tcacaccaga atcattgtga cctgtagacc tgcaaaacaa aggaccaaag 300

gttagcatgc agaagtgaaa gtgtcaataa taaccaaacc actccatcaa gttaggtctg 360

gggaaaagca gcagcaaaaa tgagttctta cttctgggca caaaatgaaa gtaacagacc 420

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tgtatgcttc attgttgttt tgggagggct tttgaagatg tgtttaaaga attgtgaagt 540

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tgttgaggtg caccaaattg tctaccctct tctaagaaca tcaagttttt cactttattc 660

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<400> 150

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20 25 30

Thr Leu Val Cys Phe Ile Val Val Leu Gly Gly Leu Leu Lys Met Cys
35 40 45

Leu Lys Asn Cys Glu Val Ile Val Leu Thr Ile Leu Ser Leu Ser Gly
50 55 60

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Phe Val Ile Gly His Met Ala Tyr Asn Ser Val Glu Val His Gln Ile
65                  70                  75                  80

Val Tyr Pro Leu Leu Arg Thr Ser Ser Phe Ser Leu Tyr Ser Tyr Phe
                85                  90                  95

Ser Pro Leu Ile Ile Phe Met Val Ala Leu Asp Val Glu Phe Tyr Thr
            100                 105                 110

Leu Lys Lys Met Phe Trp Gln Val Leu Leu Thr Gly Leu Ile Ser Phe
        115                 120                 125

Ser Thr Ala Ser Ile Ile Ile Gly Tyr Val Val Ile Lys Phe Asn Lys
    130                 135                 140

Asp Ser Trp Asp Leu Gln Ser Cys Leu Leu Phe Ser Ile Thr Leu Gly
145                 150                 155                 160

Ile Ile Asp Pro Leu Arg Ser Val Asn Ser Leu Lys Thr Ile Gly Ile
                165                 170                 175

Ser Lys Ile Tyr Ile Asp Leu Ile Arg Gly Glu Ser Leu Ile Ile Cys
            180                 185                 190

Ser Ile Ala Ser Ile Phe Phe Gly Asn Phe Arg Gly Asn Arg Ile His
        195                 200                 205

Phe Ser Ile Phe Arg Asp Leu His Val Gly Ile Glu Leu Ser Tyr Asp
    210                 215                 220

Ile Leu Gly Ser Ile Ile Phe Gly Tyr Trp Cys Ala Lys Ile Ile Gln
225                 230                 235                 240

Cys Ile Leu Ala Asp Val Phe Ser Asn Met Leu Thr Asn Ile Ile Leu
                245                 250                 255

Cys Phe Ser Met Val Tyr Met Thr Phe Tyr Ile Val Glu Phe Leu Gly
            260                 265                 270

Met Ser Gly Thr Leu Ala Leu Ala Ala Val Gly Leu Asn Leu Asp Ser
        275                 280                 285

Leu Thr Phe Lys Pro Lys Ile Glu Leu Val Ile Thr Lys Phe Leu Arg
    290                 295                 300

Ile Phe Ser Ser Val Tyr Glu His Leu Ile Tyr Ala Phe Phe Gly Ile
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305                 310                 315                 320

Val Ile Gly Cys Gly Glu Leu Ser His Tyr Glu Phe His Thr Ile Pro
                325                 330                 335

Phe Ile Phe Ile Leu Phe Thr Thr Val Asn Leu Val Arg Leu Leu Thr
            340                 345                 350

Ile Leu Leu Val Ser Pro Ile Leu Met His Ser Asn Tyr Glu Tyr Asn
        355                 360                 365

Trp Arg Trp Gly Val Val Ile Thr Trp Ser Gly Ile Lys Gly Val Phe
    370                 375                 380

Asn Leu Leu Trp Ala Pro Asp Val Tyr Asn Leu Ala Glu Arg Lys Val
385                 390                 395                 400

Glu Val Pro Gln Met Phe Ile Leu Tyr Val Gln Val Ile Ser Leu Leu
                405                 410                 415

Thr Met Gly Ile Asn Ser Tyr Val Met Thr Gln Ser Ala Arg Lys Leu
            420                 425                 430

Asp Leu Cys Val Leu Ser Leu Pro Arg Gln Met Ile Leu Gln Asn Ala
        435                 440                 445

Thr Gln His Ile Gln Glu Ile Val Gln Asn Thr Ile Thr Leu Phe Lys
    450                 455                 460

Thr Glu Lys Ile Leu Thr Asn Val Asn Trp Thr Leu Val Glu Asp Lys
465                 470                 475                 480

Thr Arg Ile Glu Tyr Ile Pro Phe Ser His Val Ser His Asn Asp Met
                485                 490                 495

Lys Thr Glu Ser Thr Thr Asp Glu Ala Leu Met Glu Glu Ala Arg Leu
            500                 505                 510

His Val Ala Ala Ile Gln Met Ser Ser Phe Glu Lys Gln Arg Asn Asn
        515                 520                 525

Gly Ile Leu Glu Ile Glu Ala Ala Arg Ile Leu Ile Gly Ala Ala Lys
    530                 535                 540

Cys Tyr Tyr Ser Ile Gln Gly Lys Phe Met Ser Ile Tyr Asp Val Ser
545                 550                 555                 560
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Thr Tyr Met Arg Thr Arg Ser Trp Leu Ile Lys Phe Lys Asn Val Leu
                565                 570                 575

Thr Phe Leu Glu Tyr Cys Ile Glu Lys Ile His Phe Ile Pro Pro Glu
            580                 585                 590

Ser Asn Thr Phe Leu Thr Phe Ile Phe His Ile Val Phe Ser Glu Glu
        595                 600                 605

Phe Glu Tyr Thr Gly Gln Ile Ile Asn Leu Ile Tyr Ile Tyr Pro Met
    610                 615                 620

Ile Ile His Leu Trp Pro Met Ala Arg Gly Leu Asn Val Ser Ala Leu
625                 630                 635                 640

Ile Ser Ile Asn Tyr Tyr Phe Met Phe Leu Tyr Val Leu Glu Ser Thr
                645                 650                 655

Leu Lys Ile Ile Ile Leu Lys Arg Lys Tyr Phe Gln Gln Cys Trp Asn
            660                 665                 670

Thr Leu Glu Phe Phe Ile Leu Val Ile Gly Ile Ile Asp Ile Phe Cys
        675                 680                 685

Val Tyr Phe Val Lys Leu Arg Pro Asp Asn Leu Ala Leu Ile Gln Leu
    690                 695                 700

Thr Val Ile Met Gly Tyr Leu Arg Ile Ile Arg Phe Leu Pro Leu Phe
705                 710                 715                 720

Lys Ile Ile Val Pro Ile Leu Ile Arg Ile Ala Asp Val Gln Ile Lys
                725                 730                 735

Lys Arg Leu Ser Leu Met Tyr Ser Ile Thr Lys Gly Tyr Ile Lys Ser
            740                 745                 750

Gln Glu Asp Ala Lys Leu Leu Ile Lys Gln Ile Ala Val Cys Glu Ser
        755                 760                 765

Ile Tyr Gln Lys Leu Cys Glu Ile Leu Glu Thr Asn Lys Gln Asp Ala
    770                 775                 780

Val Lys Glu Leu Val Leu Met Glu His Glu Gly Arg Asp Val Val Ile
785                 790                 795                 800

Ala Leu Lys Thr Lys Gln Ala Ile Arg Asn Val Ile Ala Lys Ala Leu
                805                 810                 815
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Lys Asn Leu Thr Phe Leu Cys Ser Arg Gly Ile Ile Asp Lys His Glu
            820                 825                 830

Val Ile Glu Ile Asn Lys Val Leu Leu Lys Lys Leu Lys Ala Leu Asn
        835                 840                 845

Asn Phe Pro Lys Ala Ile Pro Pro Pro Thr Pro Asp Ile Tyr Leu His
    850                 855                 860

Asn Ile Ile Trp Leu Glu Gly Lys Asp Val Leu Ile Asp Phe Phe Lys
865                 870                 875                 880

Glu Arg Ala Lys Leu Ala Cys Phe Asp Ser Gly Asp Thr Ile Cys Lys
                885                 890                 895

Gly Gly Glu Met Pro Gln Gly Ile Tyr Leu Ile Ile Ser Gly Met Ala
            900                 905                 910

Ile Leu His Ser Leu Ser Pro Thr Phe Gly Ile Glu Ser Asn Gln Arg
        915                 920                 925

Cys Asp Arg Gly Ser Arg Asp Met Phe Thr Glu Phe Cys Thr Thr Gly
    930                 935                 940

Asp Ile Ile Gly Glu Leu Ser Cys Leu Leu Lys Arg Glu Ile Glu Tyr
945                 950                 955                 960

Thr Val Ile Cys Glu Thr Ser Leu Gln Ala Cys Phe Ile Ser Leu Glu
                965                 970                 975

Asp Leu Tyr Glu Gly Phe Asp Ala Phe Trp Pro Ser Leu Glu Tyr Lys
            980                 985                 990

Ile Trp Leu Lys Leu Ala Leu Ser  Thr Ala Tyr Gln Tyr  Phe Glu Ser
        995                 1000                1005

Ser Leu  Ile Asp Glu Asp Leu  Arg Phe Gln Asn Cys  Val Met Phe
    1010                1015                1020

Asn Gln  Ala Tyr Val Glu Thr  Leu Ser Ser Tyr Ser  Asp Met Ile
    1025                1030                1035

Ile Asp  Asn Met Thr Met Lys  Phe Val Ile Ile Val  Tyr Gly Ser
    1040                1045                1050

Val Ile  Asp Thr Lys Thr Glu  Glu Pro Tyr Phe Ala  Pro Cys Ile
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1055 1060 1065

Ile Pro Thr Thr Cys Glu Gln Val Gln Gly Thr Ser Asp Leu Ser
1070 1075 1080

Lys Leu Leu Ile Ile Gln Ala Ser Glu Leu Thr Gln Arg Asn Ser
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Asn Thr Asn Val Met Ala Ser Val Asn Thr Val Phe Glu Gln Pro
1100 1105 1110

Gly Lys Asn Ile Asn Gly Arg Gln Lys Met Ser
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<223> Oligonucleotide

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cctgtttcag tggcttctaa g 21

<210> 153
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<212> DNA
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gcaatgaaaa caaatgaatt cccttctcca tgtttggact caaagactaa ggtggttatg 180

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<212> PRT
<213> Homo sapiens

<400> 154

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Val Thr Cys Arg Lys Ala Val Leu Asp Cys Glu Ala Met Lys Thr Asn
20 25 30

Glu Phe Pro Ser Pro Cys Leu Asp Ser Lys Thr Lys Val Val Met Lys
35 40 45

Gly Gln Asn Val Ser Met Phe Cys Ser His Lys Asn Lys Ser Leu Gln
50 55 60

Ile Thr Tyr Ser Leu Phe Arg Arg Lys Thr His Leu Gly Thr Gln Asp
65 70 75 80

Gly Lys Gly Glu Pro Ala Ile Phe Asn Leu Ser Ile Thr Glu Ala His
85 90 95

Glu Ser Gly Pro Tyr Lys Cys Lys Ala Gln Val Thr Ser Cys Ser Lys
100 105 110

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Tyr Ser Arg Asp Phe Ser Phe Thr Ile Val Asp Pro Val Thr Ser Pro
        115                 120                 125

Val Leu Asn Ile Met Val Ile Gln Thr Glu Thr Asp Arg His Ile Thr
    130                 135                 140

Leu His Cys Leu Ser Val Asn Gly Ser Leu Pro Ile Asn Tyr Thr Phe
145                 150                 155                 160

Phe Glu Asn His Val Ala Ile Ser Pro Ala Ile Ser Lys Tyr Asp Arg
                165                 170                 175

Glu Pro Ala Glu Phe Asn Leu Thr Lys Lys Asn Pro Gly Glu Glu Glu
            180                 185                 190

Glu Tyr Arg Cys Glu Ala Lys Asn Arg Leu Pro Asn Tyr Ala Thr Tyr
        195                 200                 205

Ser His Pro Val Thr Met Pro Ser Thr Gly Gly Asp Ser Cys Pro Phe
    210                 215                 220

Cys Leu Lys Leu Leu Leu Pro Gly Leu Leu Leu Leu Leu Val Val Ile
225                 230                 235                 240

Ile Leu Ile Leu Ala Phe Trp Val Leu Pro Lys Tyr Lys Thr Arg Lys
                245                 250                 255

Ala Met Arg Asn Asn Val Pro Arg Asp Arg Gly Asp Thr Ala Met Glu
            260                 265                 270

Val Gly Ile Tyr Ala Asn Ile Leu Glu Lys Gln Ala Lys Glu Glu Ser
        275                 280                 285

Val Pro Glu Val Gly Ser Arg Pro Cys Val Ser Thr Ala Gln Asp Glu
    290                 295                 300

Ala Lys His Ser Gln Glu Leu Gln Tyr Ala Thr Pro Val Phe Gln Glu
305                 310                 315                 320

Val Ala Pro Arg Glu Gln Glu Ala Cys Asp Ser Tyr Lys Ser Gly Tyr
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Val Tyr Ser Glu Ser
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<400> 156
acagagtgag actccatcct g 21

<210> 157
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<211> 350
<212> PRT

<213> Homo sapiens

<400> 158

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Glu Val Gly Ala Ala Ala Gly Gly Ala Gln Ala Ala Gly Pro Pro Glu
            20                  25                  30

Trp Pro Pro Gly Ser Pro Gln Ala Leu Arg Gln Pro Gly Arg Ala Arg
        35                  40                  45

Val Ala Met Ala Ala Leu Val Trp Leu Leu Ala Gly Ala Ser Met Ser
    50                  55                  60

Ser Leu Asn Lys Trp Ile Phe Thr Val His Gly Phe Gly Arg Pro Leu
65                  70                  75                  80

Leu Leu Ser Ala Leu His Met Leu Val Ala Ala Leu Ala Cys His Arg
                85                  90                  95

Gly Ala Arg Arg Pro Met Pro Gly Gly Thr Arg Cys Arg Val Leu Leu
            100                 105                 110

Leu Ser Leu Thr Phe Gly Thr Ser Met Ala Cys Gly Asn Val Gly Leu
        115                 120                 125

Arg Ala Val Pro Leu Asp Leu Ala Gln Leu Val Thr Thr Thr Thr Pro
    130                 135                 140

Leu Phe Thr Leu Ala Leu Ser Ala Leu Leu Leu Gly Arg Arg His His
145                 150                 155                 160

Pro Leu Gln Leu Ala Ala Met Gly Pro Leu Cys Leu Gly Ala Ala Cys
                165                 170                 175

Ser Leu Ala Gly Glu Phe Arg Thr Pro Pro Thr Gly Cys Gly Phe Leu
            180                 185                 190

Leu Ala Ala Thr Cys Leu Arg Gly Leu Lys Ser Val Gln Gln Ser Ala
        195                 200                 205

Leu Leu Gln Glu Glu Arg Leu Asp Ala Val Thr Leu Leu Tyr Ala Thr
    210                 215                 220

Ser Leu Pro Ser Phe Cys Leu Leu Ala Gly Ala Ala Leu Val Leu Glu
225                 230                 235                 240
```

Ala Gly Val Ala Pro Pro Pro Thr Ala Gly Asp Ser Arg Leu Trp Ala
245 250 255

Cys Ile Leu Leu Ser Cys Leu Leu Ser Val Leu Tyr Asn Leu Ala Ser
260 265 270

Phe Ser Leu Leu Ala Leu Thr Ser Ala Leu Thr Val His Val Leu Gly
275 280 285

Asn Leu Thr Val Val Gly Asn Leu Ile Leu Ser Arg Leu Leu Phe Gly
290 295 300

Ser Arg Leu Ser Ala Leu Ser Tyr Val Gly Ile Ala Leu Thr Leu Ser
305 310 315 320

Gly Met Phe Leu Tyr His Asn Cys Glu Phe Val Ala Ser Trp Ala Ala
325 330 335

Arg Arg Gly Leu Trp Arg Arg Asp Gln Pro Ser Lys Gly Leu
340 345 350

<210> 159
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 159
caagtcggtt cagcaaagtg c 21

<210> 160
<211> 21
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<220>
<223> Oligonucleotide

<400> 160
cctgaaagag tgagtgcgat g 21

<210> 161
<211> 963
<212> DNA
<213> Homo sapiens

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gactacacaa ggactgaacc agaaggaaga ggacagagca aagccatgaa catcatccta 60

gaaatccttc tgcttctgat caccatcatc tactcctact tggagtcgtt ggtgaagttt 120

ttcattcctc agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 180

catggaatag gcaggcagac tacttatgaa tttgcaaaac gacagagcat attggttctg 240

tgggatatta ataagcgcgg tgtggaggaa actgcagctg agtgccgaaa actaggcgtc 300

actgcgcatg cgtatgtggt agactgcagc aacagagaag agatctatcg ctctctaaat 360

caggtgaaga aagaagtggg tgatgtaaca atcgtggtga ataatgctgg gacagtatat 420

ccagccgatc ttctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 480

ctaggacatt tttggatcac aaaagcactt cttccatcga tgatggagag aaatcatggc 540

cacatcgtca cagtggcttc agtgtgcggc cacgaaggga ttccttacct catcccatat 600

tgttccagca aatttgccgc tgttggcttt cacagaggtc tgacatcaga acttcaggcc 660

ttgggaaaaa ctggtatcaa aacctcatgt ctctgcccag tttttgtgaa tactgggttc 720

accaaaaatc caagcacaag attatggcct gtattggaga cagatgaagt cgtaagaagt 780

ctgatagatg gaatacttac caataagaaa atgatttttg ttccatcgta tatcaatatc 840

tttctgagac tacagaatcc tgataatatt aaaaacattg gtttggcact agcagcagtc 900

aaacgaacaa gattaattac ctgtcttcct gtttctcaag aatatttacg tagtttttca 960

tag 963

<210> 162
<211> 305
<212> PRT
<213> Homo sapiens

<400> 162

Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Leu Ile Thr Ile Ile Tyr
1 5 10 15

Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys
20 25 30

Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
35 40 45

Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln Ser Ile Leu Val
50 55 60

Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu Thr Ala Ala Glu Cys
65 70 75 80

Arg Lys Leu Gly Val Thr Ala His Ala Tyr Val Val Asp Cys Ser Asn
85 90 95

```
Arg Glu Glu Ile Tyr Arg Ser Leu Asn Gln Val Lys Lys Glu Val Gly
            100                 105                 110

Asp Val Thr Ile Val Val Asn Asn Ala Gly Thr Val Tyr Pro Ala Asp
        115                 120                 125

Leu Leu Ser Thr Lys Asp Glu Glu Ile Thr Lys Thr Phe Glu Val Asn
    130                 135                 140

Ile Leu Gly His Phe Trp Ile Thr Lys Ala Leu Leu Pro Ser Met Met
145                 150                 155                 160

Glu Arg Asn His Gly His Ile Val Thr Val Ala Ser Val Cys Gly His
                165                 170                 175

Glu Gly Ile Pro Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala
            180                 185                 190

Val Gly Phe His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys
        195                 200                 205

Thr Gly Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly
    210                 215                 220

Phe Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp
225                 230                 235                 240

Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys Met
                245                 250                 255

Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln Asn Pro
            260                 265                 270

Asp Asn Ile Lys Asn Ile Gly Leu Ala Leu Ala Ala Val Lys Arg Thr
        275                 280                 285

Arg Leu Ile Thr Cys Leu Pro Val Ser Gln Glu Tyr Leu Arg Ser Phe
    290                 295                 300

Ser
305
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<210> 163
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 163
ggtctgacat cagaacttca g 21

<210> 164
<211> 21
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<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 164
tgcatacatc tctggctgga g 21

<210> 165
<211> 6014
<212> DNA
<213> Homo sapiens

<400> 165
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gcagtgtgtc cggctgacgg tccatcccaa caatatctcc gtctctcagt acaacgtgct 120

gctggtcctg gagacgtaca atgtcccgga gctgtcagct ggcgtcaact gcacctttga 180

ggacctgtca gagatggatg ggctggtcgt gggcaatcag atccagtgct actcccctgc 240

agccaaggag gtgccccgga tcatcacaga gaatggggac caccatgtcg tacagcttca 300

gctcaaatca aaggagaccg gcatgacctt cgccagcacc agctttgtct tctacaattg 360

cagcgtccac aattcgtgcc tgtcctgcgt ggagagtcca taccgctgcc actggtgtaa 420

ataccggcat gtctgcaccc atgaccccaa gacctgctcc ttccaggaag gccgagtgaa 480

gctgcccgag gactgccccc agctgctgcg agtggacaag atcctggtgc ccgtggaggt 540

gatcaagcct atcacgctga aggccaagaa cctcccccag ccccagtctg ggcagcgtgg 600

ctacgaatgc atcctcaaca ttcagggcag cgagcagcga gtgcccgccc tgcgcttcaa 660

cagctccagc gtacagtgcc agaacacctc ttattcctat gaagggatgg agatcaacaa 720

cctgcccgtg gagttgacag tcgtgtggaa tgggcacttc aacattgaca acccagctca 780

gaataaagtt cacctctaca agtgtggagc catgcgtgag agctgcgggc tgtgcctcaa 840

ggctgaccca gacttcgcat gtggctggtg ccagggccca ggccagtgca ccctgcgcca 900

gcactgccct gcccaggaga gccagtggct ggagctgtct ggtgccaaaa gcaagtgcac 960

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cactatccga ggggagaacc tgggcctgga atttcgcgac atcgcctccc atgtcaaggt 1080

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ccacaggcga tctccatcct acattgtctg caacaccaca tcctcagatg aggtgctaga 1440

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agacttatca cggt 6014

<210> 166
<211> 817
<212> PRT
<213> Homo sapiens

<400> 166

Met Lys Gln Cys Val Arg Leu Thr Val His Pro Asn Asn Ile Ser Val
1 5 10 15

Ser Gln Tyr Asn Val Leu Leu Val Leu Glu Thr Tyr Asn Val Pro Glu
20 25 30

Leu Ser Ala Gly Val Asn Cys Thr Phe Glu Asp Leu Ser Glu Met Asp
35 40 45

Gly Leu Val Val Gly Asn Gln Ile Gln Cys Tyr Ser Pro Ala Ala Lys
50 55 60

```
Glu Val Pro Arg Ile Ile Thr Glu Asn Gly Asp His His Val Val Gln
65                  70                  75                  80

Leu Gln Leu Lys Ser Lys Glu Thr Gly Met Thr Phe Ala Ser Thr Ser
                85                  90                  95

Phe Val Phe Tyr Asn Cys Ser Val His Asn Ser Cys Leu Ser Cys Val
            100                 105                 110

Glu Ser Pro Tyr Arg Cys His Trp Cys Lys Tyr Arg His Val Cys Thr
        115                 120                 125

His Asp Pro Lys Thr Cys Ser Phe Gln Glu Gly Arg Val Lys Leu Pro
    130                 135                 140

Glu Asp Cys Pro Gln Leu Leu Arg Val Asp Lys Ile Leu Val Pro Val
145                 150                 155                 160

Glu Val Ile Lys Pro Ile Thr Leu Lys Ala Lys Asn Leu Pro Gln Pro
                165                 170                 175

Gln Ser Gly Gln Arg Gly Tyr Glu Cys Ile Leu Asn Ile Gln Gly Ser
            180                 185                 190

Glu Gln Arg Val Pro Ala Leu Arg Phe Asn Ser Ser Ser Val Gln Cys
        195                 200                 205

Gln Asn Thr Ser Tyr Ser Tyr Glu Gly Met Glu Ile Asn Asn Leu Pro
    210                 215                 220

Val Glu Leu Thr Val Val Trp Asn Gly His Phe Asn Ile Asp Asn Pro
225                 230                 235                 240

Ala Gln Asn Lys Val His Leu Tyr Lys Cys Gly Ala Met Arg Glu Ser
                245                 250                 255

Cys Gly Leu Cys Leu Lys Ala Asp Pro Asp Phe Ala Cys Gly Trp Cys
            260                 265                 270

Gln Gly Pro Gly Gln Cys Thr Leu Arg Gln His Cys Pro Ala Gln Glu
        275                 280                 285

Ser Gln Trp Leu Glu Leu Ser Gly Ala Lys Ser Lys Cys Thr Asn Pro
    290                 295                 300

Arg Ile Thr Glu Ile Ile Pro Val Thr Gly Pro Arg Glu Gly Gly Thr
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305 310 315 320

Lys Val Thr Ile Arg Gly Glu Asn Leu Gly Leu Glu Phe Arg Asp Ile
325 330 335

Ala Ser His Val Lys Val Ala Gly Val Glu Cys Ser Pro Leu Val Asp
340 345 350

Gly Tyr Ile Pro Ala Glu Gln Ile Val Cys Glu Met Gly Glu Ala Lys
355 360 365

Pro Ser Gln His Ala Gly Phe Val Glu Ile Cys Val Ala Val Cys Arg
370 375 380

Pro Glu Phe Met Ala Arg Ser Ser Gln Leu Tyr Tyr Phe Met Thr Leu
385 390 395 400

Thr Leu Ser Asp Leu Lys Pro Ser Arg Gly Pro Met Ser Gly Gly Thr
405 410 415

Gln Val Thr Ile Thr Gly Thr Asn Leu Asn Ala Gly Ser Asn Val Val
420 425 430

Val Met Phe Gly Lys Gln Pro Cys Leu Phe His Arg Arg Ser Pro Ser
435 440 445

Tyr Ile Val Cys Asn Thr Thr Ser Ser Asp Glu Val Leu Glu Met Lys
450 455 460

Val Ser Val Gln Val Asp Arg Ala Lys Ile His Gln Asp Leu Val Phe
465 470 475 480

Gln Tyr Val Glu Asp Pro Thr Ile Val Arg Ile Glu Pro Glu Trp Ser
485 490 495

Ile Val Ser Gly Asn Thr Pro Ile Ala Val Trp Gly Thr His Leu Asp
500 505 510

Leu Ile Gln Asn Pro Gln Ile Arg Ala Lys His Gly Gly Lys Glu His
515 520 525

Ile Asn Ile Cys Glu Val Leu Asn Ala Thr Glu Met Thr Cys Gln Ala
530 535 540

Pro Ala Leu Ala Leu Gly Pro Asp His Gln Ser Asp Leu Thr Glu Arg
545 550 555 560

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Pro Glu Glu Phe Gly Phe Ile Leu Asp Asn Val Gln Ser Leu Leu Ile
                565                 570                 575

Leu Asn Lys Thr Asn Phe Thr Tyr Tyr Pro Asn Pro Val Phe Glu Ala
            580                 585                 590

Phe Gly Pro Ser Gly Ile Leu Glu Leu Lys Pro Gly Thr Pro Ile Ile
        595                 600                 605

Leu Lys Gly Lys Asn Leu Ile Pro Pro Val Ala Gly Gly Asn Val Lys
    610                 615                 620

Leu Asn Tyr Thr Val Leu Val Gly Glu Lys Pro Cys Thr Val Thr Val
625                 630                 635                 640

Ser Asp Val Gln Leu Leu Cys Glu Ser Pro Asn Leu Ile Gly Arg His
                645                 650                 655

Lys Val Met Ala Arg Val Gly Gly Met Glu Tyr Ser Pro Gly Met Val
            660                 665                 670

Tyr Ile Ala Pro Asp Ser Pro Leu Ser Leu Pro Ala Ile Val Ser Ile
        675                 680                 685

Ala Val Ala Gly Gly Leu Leu Ile Ile Phe Ile Val Ala Val Leu Ile
    690                 695                 700

Ala Tyr Lys Arg Lys Ser Arg Glu Ser Asp Leu Thr Leu Lys Arg Leu
705                 710                 715                 720

Gln Met Gln Met Asp Asn Leu Glu Ser Arg Val Ala Leu Glu Cys Lys
                725                 730                 735

Glu Gly Thr Glu Trp Pro His Ala Gly Gly His Val Cys Val Arg Val
            740                 745                 750

Cys Ile Cys Val Cys Met His Ile Cys Val Cys Val Cys Ile Cys Phe
        755                 760                 765

Ile Tyr Lys Gln Ala Gly Trp Ala Ala Val Gly Ser Ala Gly Gly Trp
    770                 775                 780

Arg Cys Val Cys Leu Cys Glu Cys Val Cys Val His Val Cys Val Cys
785                 790                 795                 800

Thr Ser Val Cys Ile Tyr Val Ser Tyr Thr Ser Lys Gln Ala Gly Gln
                805                 810                 815
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Gln

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<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 167
gcaccaaggt cactatccga g 21

<210> 168
<211> 21
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<220>
<223> Oligonucleotide

<400> 168
tctgagagag tcagtgtcat g 21

<210> 169
<211> 2565
<212> DNA
<213> Homo sapiens

<400> 169
actgcgacgg taccggggcg gcggggaagg accgagaggc gggaggagca gcggctcagg 60

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cgctgggctg ctcttcctga ggttttccta agccatcccc tggcggaacc gcccccagta 180

tggactccaa ttgccttgac agtgttttta gtggctgttg caacattatg taaagaacaa 240

ggaataacag ttgtaggaat ttgctgtgtg tatgaagtgt ttattgccca ggggtatact 300

ttgccattac tatgtactac tgctggacag tttctccgtg gaaagggtag cattccattt 360

tctatgctgc agacactagt aaaactcatt gtcttgatgt tcagtacatt attacttgtt 420

gtgattagag tccaggttat tcaatcccaa cttccagtat tcaccaggtt tgataaccca 480

gctgctgtaa gcccaactcc tacaaggcaa ctaactttta actacctcct tcctgtgaat 540

gcttggttgt tattaaatcc ttcagagctc tgctgtgatt ggaccatggg aacaatacca 600

cttatagagt cattactaga tattcgaaat ctggccacat ttactttctt ttgttttctg 660

gggatgttgg gagtattcag tatcagatac tctggtgatt cctccaagac tgttttaatg 720

ttgcctgcta aaactgacat gggtcaaaaa tttgagaaaa gtagtgaaga ttcaaagcag 780

tcaagaagag tggaaggaac tttccagaga aacctagaaa tcccaaacag tcttaaggat 840

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tctctagcag tgcgttgcca ctctgttgga tttgttgttg ccgagcgagt attatatgtt 960

cccagcatgg ggttctgtat tttggtagcc catggatggc agaaaatatc aacaaaaagt 1020

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gaatcttaca tgatggctaa atcactgatg cctcaaatta ttcctggtaa aaaatatgca 1380

gccagaattg cccctaacca cctaaatgtt tatatcaatc tggctaacct gatccgagca 1440

aatgagtccc gactggaaga agcagatcag ctgtaccgtc aagcaataag catgaggccc 1500

gacttcaagc aggcttacat tagcagagga gaattgcttt taaaaatgaa taaacctctt 1560

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tacaacttgg caattgtaca tattgaactt aaagaaccaa atgaagccct aaaaaacttt 1680

aatcgtgctc tggaactaaa tccaaagcat aaactagcat tattcaactc tgctatagta 1740

atgcaagaat caggtgaggt taaactcaga cctgaagcta gaaaacgact tctaagttat 1800

ataaatgaag agccactaga tgctaatggg tatttcaatt tgggaatgct tgccatggat 1860

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gctttgccaa ttttggagga gttactcaga tactaccctg atcatatcaa gggcctcatt 2040

ttaaaaggag acattctgat gaatcaaaag aaagatatac taggagcaaa aaaatgtttt 2100

gaaaggattt tggagatgga tccaagcaat gtgcaaggaa aacacaatct ttgtgttgtt 2160

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<212> PRT

<213> Homo sapiens

<400> 170

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Leu Leu Val Val Ile Arg Val Gln Val Ile Gln Ser Gln Leu Pro Val
            20                  25                  30

Phe Thr Arg Phe Asp Asn Pro Ala Ala Val Ser Pro Thr Pro Thr Arg
        35                  40                  45

Gln Leu Thr Phe Asn Tyr Leu Leu Pro Val Asn Ala Trp Leu Leu Leu
    50                  55                  60

Asn Pro Ser Glu Leu Cys Cys Asp Trp Thr Met Gly Thr Ile Pro Leu
65                  70                  75                  80

Ile Glu Ser Leu Leu Asp Ile Arg Asn Leu Ala Thr Phe Thr Phe Phe
                85                  90                  95

Cys Phe Leu Gly Met Leu Gly Val Phe Ser Ile Arg Tyr Ser Gly Asp
            100                 105                 110

Ser Ser Lys Thr Val Leu Met Leu Pro Ala Lys Thr Asp Met Gly Gln
        115                 120                 125

Lys Phe Glu Lys Ser Ser Glu Asp Ser Lys Gln Ser Arg Arg Val Glu
    130                 135                 140

Gly Thr Phe Gln Arg Asn Leu Glu Ile Pro Asn Ser Leu Lys Asp Lys
145                 150                 155                 160

Phe Glu Leu Gly Ala His Ala Phe Met Thr Val Leu Ile Cys Ser Ala
                165                 170                 175

Leu Gly Leu Ser Leu Ala Val Arg Cys His Ser Val Gly Phe Val Val
            180                 185                 190

Ala Glu Arg Val Leu Tyr Val Pro Ser Met Gly Phe Cys Ile Leu Val
        195                 200                 205

Ala His Gly Trp Gln Lys Ile Ser Thr Lys Ser Val Phe Lys Lys Leu
    210                 215                 220

Ser Trp Ile Cys Leu Ser Met Val Ile Leu Thr His Ser Leu Lys Thr
225                 230                 235                 240
```

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Phe His Arg Asn Trp Asp Trp Glu Ser Glu Tyr Thr Leu Phe Met Ser
               245                 250                 255

Ala Leu Lys Val Asn Lys Asn Asn Ala Lys Leu Trp Asn Asn Val Gly
           260                 265                 270

His Ala Leu Glu Asn Glu Lys Asn Phe Glu Arg Ala Leu Lys Tyr Phe
       275                 280                 285

Leu Gln Ala Thr His Val Gln Pro Asp Asp Ile Gly Ala His Met Asn
   290                 295                 300

Val Gly Arg Thr Tyr Lys Asn Leu Asn Arg Thr Lys Glu Ala Glu Glu
305                 310                 315                 320

Ser Tyr Met Met Ala Lys Ser Leu Met Pro Gln Ile Ile Pro Gly Lys
               325                 330                 335

Lys Tyr Ala Ala Arg Ile Ala Pro Asn His Leu Asn Val Tyr Ile Asn
           340                 345                 350

Leu Ala Asn Leu Ile Arg Ala Asn Glu Ser Arg Leu Glu Glu Ala Asp
       355                 360                 365

Gln Leu Tyr Arg Gln Ala Ile Ser Met Arg Pro Asp Phe Lys Gln Ala
   370                 375                 380

Tyr Ile Ser Arg Gly Glu Leu Leu Leu Lys Met Asn Lys Pro Leu Lys
385                 390                 395                 400

Ala Lys Glu Ala Tyr Leu Lys Ala Leu Glu Leu Asp Arg Asn Asn Ala
               405                 410                 415

Asp Leu Trp Tyr Asn Leu Ala Ile Val His Ile Glu Leu Lys Glu Pro
           420                 425                 430

Asn Glu Ala Leu Lys Asn Phe Asn Arg Ala Leu Glu Leu Asn Pro Lys
       435                 440                 445

His Lys Leu Ala Leu Phe Asn Ser Ala Ile Val Met Gln Glu Ser Gly
   450                 455                 460

Glu Val Lys Leu Arg Pro Glu Ala Arg Lys Arg Leu Leu Ser Tyr Ile
465                 470                 475                 480

Asn Glu Glu Pro Leu Asp Ala Asn Gly Tyr Phe Asn Leu Gly Met Leu
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485 490 495

Ala Met Asp Asp Lys Lys Asp Asn Glu Ala Glu Ile Trp Met Lys Lys
500 505 510

Ala Ile Lys Leu Gln Ala Asp Phe Arg Ser Ala Leu Phe Asn Leu Ala
515 520 525

Leu Leu Tyr Ser Gln Thr Ala Lys Glu Leu Lys Ala Leu Pro Ile Leu
530 535 540

Glu Glu Leu Leu Arg Tyr Tyr Pro Asp His Ile Lys Gly Leu Ile Leu
545 550 555 560

Lys Gly Asp Ile Leu Met Asn Gln Lys Lys Asp Ile Leu Gly Ala Lys
565 570 575

Lys Cys Phe Glu Arg Ile Leu Glu Met Asp Pro Ser Asn Val Gln Gly
580 585 590

Lys His Asn Leu Cys Val Val Tyr Phe Glu Glu Lys Asp Leu Leu Lys
595 600 605

Ala Glu Arg Cys Leu Leu Glu Thr Leu Ala Leu Ala Pro His Glu Glu
610 615 620

Tyr Ile Gln Arg His Leu Asn Ile Val Arg Asp Lys Ile Ser Ser Ser
625 630 635 640

Ser Phe Ile Glu Pro Ile Phe Pro Thr Ser Lys Ile Ser Ser Val Glu
645 650 655

Gly Lys Lys Ile Pro Thr Glu Ser Val Lys Glu Ile Arg Gly Glu Ser
660 665 670

Arg Gln Thr Gln Ile Val Lys Thr Ser Asp Asn Lys Ser Gln Ser Lys
675 680 685

Ser Asn Lys Gln Leu Gly Lys Asn Gly Asp Glu Glu Thr Pro His Lys
690 695 700

Thr Thr Lys Asp Ile Lys Glu Ile Glu Lys Lys Arg Val Ala Ala Leu
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Lys Arg Leu Glu Glu Ile Glu Arg Ile Leu Asn Gly Glu
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<223> Oligonucleotide

<400> 171
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<210> 172
<211> 21
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<220>
<223> Oligonucleotide

<400> 172
cgttttctag cttcaggtct g 21

<210> 173
<211> 3296
<212> DNA
<213> Homo sapiens

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aaggtaaatg tttaagcaca cagtgaactt cctgaggccc ccaaatctaa tggaactagc 180

tattgagggc taaaagagga tggttttttt agaaaactcg aagcaaatct ctcaggctgg 240

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taaatgaagc taaaactttg ttctaataaa tttaatcttt acagcaacct atgaggtaga 360

taatattgtc attcccatga gggagctaag gatcagagaa ggtaagtcac ttgtctaagg 420

tcacatagct agcatgttat gcaatcagga gtcaaacctg gtttgtctga atctgaagtc 480

catctgctct gtgcactttt ataccgtctg ctttttcctt tattcctaac cttcttccat 540

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gccctagtca cctggctttg cctttgccct gctgtgtgat cttagctccc tgcccaggcc 660

cacagccatg gccatggccc agaaactcag ccacctcctg ccgagtctgc ggcaggtcat 720

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<210> 174
<211> 346
<212> PRT
<213> Homo sapiens

<400> 174

Met Ala Met Ala Gln Lys Leu Ser His Leu Leu Pro Ser Leu Arg Gln
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Val Ile Gln Glu Pro Gln Leu Ser Leu Gln Pro Glu Pro Val Phe Thr
20 25 30

Val Asp Arg Ala Glu Val Pro Pro Leu Phe Trp Lys Pro Tyr Ile Tyr
35 40 45

Ala Gly Tyr Arg Pro Leu His Gln Thr Trp Arg Phe Tyr Phe Arg Thr
50 55 60

Leu Phe Gln Gln His Asn Glu Ala Val Asn Val Trp Thr His Leu Leu
65 70 75 80

Ala Ala Leu Val Leu Leu Leu Arg Leu Ala Leu Phe Val Glu Thr Val
85 90 95

Asp Phe Trp Gly Asp Pro His Ala Leu Pro Leu Phe Ile Ile Val Leu
100 105 110

Ala Ser Phe Thr Tyr Leu Ser Phe Ser Ala Leu Ala His Leu Leu Gln
115 120 125

Ala Lys Ser Glu Phe Trp His Tyr Ser Phe Phe Phe Leu Asp Tyr Val
130 135 140

Gly Val Ala Val Tyr Gln Phe Gly Ser Ala Leu Ala His Phe Tyr Tyr
145 150 155 160

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Ala Ile Glu Pro Ala Trp His Ala Gln Val Gln Ala Val Phe Leu Pro
                165                 170                 175

Met Ala Ala Phe Leu Ala Trp Leu Ser Cys Ile Gly Ser Cys Tyr Asn
            180                 185                 190

Lys Tyr Ile Gln Lys Pro Gly Leu Leu Gly Arg Thr Cys Gln Glu Val
        195                 200                 205

Pro Ser Val Leu Ala Tyr Ala Leu Asp Ile Ser Pro Val Val His Arg
    210                 215                 220

Ile Phe Val Ser Ser Asp Pro Thr Thr Asp Asp Pro Ala Leu Leu Tyr
225                 230                 235                 240

His Lys Cys Gln Val Val Phe Phe Leu Leu Ala Ala Ala Phe Phe Ser
                245                 250                 255

Thr Phe Met Pro Glu Arg Trp Phe Pro Gly Ser Cys His Val Phe Gly
            260                 265                 270

Gln Gly His Gln Leu Phe His Ile Phe Leu Val Leu Cys Thr Leu Ala
        275                 280                 285

Gln Leu Glu Ala Val Ala Leu Asp Tyr Glu Ala Arg Arg Pro Ile Tyr
    290                 295                 300

Glu Pro Leu His Thr His Trp Pro His Asn Phe Ser Gly Leu Phe Leu
305                 310                 315                 320

Leu Thr Val Gly Ser Ser Ile Leu Thr Ala Phe Leu Leu Ser Gln Leu
                325                 330                 335

Val Gln Arg Lys Leu Asp Gln Lys Thr Lys
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<211> 2858
<212> DNA
<213> Homo sapiens

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tcaggccgcg gggccagggc gggccggccg gcggggcatt taaaccccgc tgacagccag 180

tccagcccgg gacacgcgcc cagctctgta gcctcctccg tcgactcagc cttaggtacc 240

ggtcaggcaa aatgcggtcc tccctggctc cgggagtctg gttcttccgg gccttctcca 300

gggacagctg gttccgaggc ctcatcctgc tgctgacctt cctaatttac gcctgctatc 360

acatgtccag gaagcctatc agtatcgtca agagccgtct gcaccagaac tgctcggagc 420

agatcaaacc catcaatgat actcacagtc tcaatgacac catgtggtgc agctgggccc 480

catttgacaa ggacaactat aaggagttac tagggggcgt ggacaacgcc ttcctcatcg 540

cctatgccat cggcatgttc atcagtgggg tttttgggga gcggcttccg ctccgttact 600

acctctcagc tggaatgctg ctcagtggcc ttttcacctc gctctttggc ctgggatatt 660

tctggaacat ccacgagctc tggtactttg tggtcatcca ggtctgtaat ggactcgtcc 720

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ttactgccgt catgggcgtc atcaccttcc tcttcctcat cgaacaccca gaagatgtgg 960

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ctttattgaa cattagccag cccagcccag accccagggc tgcctaagga cacagagatt 1920

ctccatggga aggggactgc caagcatgag gaaatagaag attcaggggc ctgagctctg 1980

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gcctggaaaa tgggcatctc tccttcccat gttaagcttt aacctctgta atctgcctgt 2160

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<210> 176
<211> 501
<212> PRT
<213> Homo sapiens

<400> 176

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Arg Asp Ser Trp Phe Arg Gly Leu Ile Leu Leu Leu Thr Phe Leu Ile
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Tyr Ala Cys Tyr His Met Ser Arg Lys Pro Ile Ser Ile Val Lys Ser
35 40 45

Arg Leu His Gln Asn Cys Ser Glu Gln Ile Lys Pro Ile Asn Asp Thr
50 55 60

His Ser Leu Asn Asp Thr Met Trp Cys Ser Trp Ala Pro Phe Asp Lys
65 70 75 80

Asp Asn Tyr Lys Glu Leu Leu Gly Gly Val Asp Asn Ala Phe Leu Ile
85 90 95

Ala Tyr Ala Ile Gly Met Phe Ile Ser Gly Val Phe Gly Glu Arg Leu
100 105 110

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Pro Leu Arg Tyr Tyr Leu Ser Ala Gly Met Leu Leu Ser Gly Leu Phe
        115                 120                 125

Thr Ser Leu Phe Gly Leu Gly Tyr Phe Trp Asn Ile His Glu Leu Trp
    130                 135                 140

Tyr Phe Val Val Ile Gln Val Cys Asn Gly Leu Val Gln Thr Thr Gly
145                 150                 155                 160

Trp Pro Ser Val Val Thr Cys Val Gly Asn Trp Phe Gly Lys Gly Lys
                165                 170                 175

Arg Gly Phe Ile Met Gly Ile Trp Asn Ser His Thr Ser Val Gly Asn
            180                 185                 190

Ile Leu Gly Ser Leu Ile Ala Gly Ile Trp Val Asn Gly Gln Trp Gly
        195                 200                 205

Leu Ser Phe Ile Val Pro Gly Ile Ile Thr Ala Val Met Gly Val Ile
    210                 215                 220

Thr Phe Leu Phe Leu Ile Glu His Pro Glu Asp Val Asp Cys Ala Pro
225                 230                 235                 240

Pro Gln His His Gly Glu Pro Ala Glu Asn Gln Asp Asn Pro Glu Asp
                245                 250                 255

Pro Gly Asn Ser Pro Cys Ser Ile Arg Glu Ser Gly Leu Glu Thr Val
            260                 265                 270

Ala Lys Cys Ser Lys Gly Pro Cys Glu Glu Pro Ala Ala Ile Ser Phe
        275                 280                 285

Phe Gly Ala Leu Arg Ile Pro Gly Val Val Glu Phe Ser Leu Cys Leu
    290                 295                 300

Leu Phe Ala Lys Leu Val Ser Tyr Thr Phe Leu Tyr Trp Leu Pro Leu
305                 310                 315                 320

Tyr Ile Ala Asn Val Ala His Phe Ser Ala Lys Glu Ala Gly Asp Leu
                325                 330                 335

Ser Thr Leu Phe Asp Val Gly Gly Ile Ile Gly Gly Ile Val Ala Gly
            340                 345                 350

Leu Val Ser Asp Tyr Thr Asn Gly Arg Ala Thr Thr Cys Cys Val Met
        355                 360                 365
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Leu Ile Leu Ala Ala Pro Met Met Phe Leu Tyr Asn Tyr Ile Gly Gln
370 375 380

Asp Gly Ile Ala Ser Ser Ile Val Met Leu Ile Ile Cys Gly Gly Leu
385 390 395 400

Val Asn Gly Pro Tyr Ala Leu Ile Thr Thr Ala Val Ser Ala Asp Leu
405 410 415

Gly Thr His Lys Ser Leu Lys Gly Asn Ala Lys Ala Leu Ser Thr Val
420 425 430

Thr Ala Ile Ile Asp Gly Thr Gly Ser Ile Gly Ala Ala Leu Gly Pro
435 440 445

Leu Leu Ala Gly Leu Ile Ser Pro Thr Gly Trp Asn Asn Val Phe Tyr
450 455 460

Met Leu Ile Ser Ala Asp Val Leu Ala Cys Leu Leu Leu Cys Arg Leu
465 470 475 480

Val Tyr Lys Glu Ile Leu Ala Trp Lys Val Ser Leu Ser Arg Gly Ser
485 490 495

Gly Tyr Lys Glu Ile
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<213> Artificial Sequence

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<400> 178
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<210> 179

<211> 4892
<212> DNA
<213> Homo sapiens

<400> 179
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cttcttggca caggtaggaa aggatgatat tacaagggtc aaaatggggg taaacagaag 180

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20 25 30

Ala Ile Phe Cys Ser Ser Leu Leu Asp Ser Val Pro Gln Lys Val Glu
35 40 45

Phe Phe Ile Asn Tyr Ser Ser Trp Gly Leu Met Pro Val Gly Phe Asp
50 55 60

Gln Trp Val Thr Pro Ser Val Asp Trp Arg Met Glu Lys Glu Lys Arg
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Leu Gly Tyr Val Ser Pro Pro Leu Phe Leu Leu Leu Ala Gly Phe
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<212> PRT
<213> Homo sapiens

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Ile Asp Val Arg Val Val Gln Ala Ala Pro Leu Arg Cys Asp Ser Thr
35 40 45

Pro Pro Glu Gly Ala Val Gly Asp Ile Cys Lys Lys Glu Asp Ala Gly
50 55 60

Asn Met Pro Ser Thr Ser Glu Gly Ser Ile Tyr Pro Glu Met Ala His
65 70 75 80

Phe Leu Arg Asn Lys Leu Ala Gly Ser Ser Val Arg Lys Pro Asp Ser
85 90 95

Gly Phe Leu Trp Glu Gly Ala Leu Arg Ala Trp Leu Phe Leu Ile Leu
100 105 110

Ile Val Leu Thr His Ile Met Trp Val Pro Leu Val Gln Val Ser Pro
115 120 125

Asn Ala Pro Leu Phe His Tyr Ile Glu Ser Ile Ala His Asp Leu Gly
130 135 140

Pro Pro Ile Gly Ala Ile Phe Leu Leu Ser Ile Ser Trp Ser Ile Val
145 150 155 160

Lys Glu Pro Met Ser Arg
165

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<213> Artificial Sequence

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<210> 186
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<223> Oligonucleotide

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ggcccgtaat gctcc 15

<210> 187
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<212> DNA
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<212> PRT
<213> Homo sapiens

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Asn Arg His Leu Glu Asp Phe Pro Ile Pro Val Pro Val Ile Leu Phe
35 40 45

Leu Leu Gly Cys Ser Phe Glu Val Leu Ser Phe Thr Ser Ser Gln Val
50 55 60

Gln Arg Tyr Ala Asn Ala Ile Gln Trp Met Ser Pro Asp Leu Phe Phe
65 70 75 80

Arg Ile Phe Thr Pro Val Val Phe Phe Thr Thr Ala Phe Asp Met Asp
85 90 95

Thr Tyr Met Leu Gln Lys Leu Phe Trp Gln Ile Leu Leu Ile Ser Ile
100 105 110

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Pro Gly Phe Leu Val Asn Tyr Ile Leu Val Leu Trp His Leu Ala Ser
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Val Asn Gln Leu Leu Leu Lys Pro Thr Gln Trp Leu Leu Phe Ser Ala
    130                 135                 140

Ile Leu Val Ser Ser Asp Pro Met Leu Thr Ala Ala Ala Ile Arg Asp
145                 150                 155                 160

Leu Gly Leu Ser Arg Ser Leu Ile Ser Leu Ile Asn Gly Glu Ser Leu
                165                 170                 175

Met Thr Ser Val Ile Ser Leu Ile Thr Phe Thr Ser Ile Met Asp Phe
            180                 185                 190

Asp Gln Arg Leu Gln Ser Lys Arg Asn His Thr Leu Ala Glu Glu Ile
        195                 200                 205

Val Gly Gly Ile Cys Ser Tyr Ile Ile Ala Ser Phe Leu Phe Gly Ile
    210                 215                 220

Leu Ser Ser Lys Leu Ile Gln Phe Trp Met Ser Thr Val Phe Gly Asp
225                 230                 235                 240

Asp Val Asn His Ile Ser Leu Ile Phe Ser Ile Leu Tyr Leu Ile Phe
                245                 250                 255

Tyr Ile Cys Glu Leu Val Gly Met Ser Gly Ile Phe Thr Leu Ala Ile
            260                 265                 270

Val Gly Leu Leu Leu Asn Ser Thr Ser Phe Lys Ala Ala Ile Glu Glu
        275                 280                 285

Thr Leu Leu Leu Glu Phe Leu Thr Leu Leu Leu Ile Ser Pro Val Leu
    290                 295                 300

Ser Arg Val Gly His Glu Phe Ser Trp Arg Trp Ile Phe Ile Met Val
305                 310                 315                 320

Cys Ser Glu Met Lys Gly Met Pro Asn Ile Asn Met Ala Leu Leu Leu
                325                 330                 335

Ala Tyr Ser Asp Leu Tyr Phe Gly Ser Asp Lys Glu Lys Ser Gln Ile
            340                 345                 350

Leu Phe His Gly Val Leu Val Cys Leu Ile Thr Leu Val Val Asn Arg
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355 360 365

Phe Ile Leu Pro Val Ala Val Thr Ile Leu Gly Leu Arg Asp Ala Thr
370 375 380

Ser Thr Lys Tyr Lys Ser Val Cys Cys Thr Phe Gln His Phe Gln Glu
385 390 395 400

Leu Thr Lys Ser Ala Ala Ser Ala Leu Lys Phe Asp Lys Asp Leu Ala
405 410 415

Asn Ala Asp Trp Asn Met Ile Glu Lys Ala Ile Thr Leu Glu Asn Pro
420 425 430

Tyr Met Leu Asn Glu Glu Glu Thr Thr Glu His Gln Lys Val Lys Cys
435 440 445

Pro His Cys Asn Lys Glu Ile Asp Glu Ile Phe Asn Thr Glu Ala Met
450 455 460

Glu Leu Ala Asn Arg Arg Leu Leu Ser Ala Gln Ile Ala Ser Tyr Gln
465 470 475 480

Arg Gln Tyr Arg Asn Glu Ile Leu Ser Gln Ser Ala Val Gln Val Leu
485 490 495

Val Gly Ala Ala Glu Ser Phe Gly Glu Lys Lys Gly Lys Cys Met Ser
500 505 510

Leu Asp Thr Ile Lys Asn Tyr Ser Glu Ser Gln Lys Thr Val Thr Phe
515 520 525

Ala Arg Lys Leu Leu Leu Asn Trp Val Tyr Asn Thr Arg Lys Glu Lys
530 535 540

Glu Gly Pro Ser Lys Tyr Phe Phe Phe Arg Ile Cys His Thr Ile Val
545 550 555 560

Phe Thr Glu Glu Phe Glu His Val Gly Tyr Leu Val Ile Leu Met Asn
565 570 575

Ile Phe Pro Phe Ile Ile Ser Trp Ile Ser Gln Leu Asn Val Ile Tyr
580 585 590

His Ser Glu Leu Lys His Thr Asn Tyr Cys Phe Leu Thr Leu Tyr Ile
595 600 605

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Leu Glu Ala Leu Leu Lys Ile Ala Ala Met Arg Lys Asp Phe Phe Ser
    610                 615                 620

His Ala Trp Asn Ile Phe Glu Leu Ala Ile Thr Leu Ile Gly Ile Leu
625                 630                 635                 640

His Val Ile Leu Ile Glu Ile Asp Thr Ile Lys Tyr Ile Phe Asn Glu
                645                 650                 655

Thr Glu Val Ile Val Phe Ile Lys Val Val Gln Phe Phe Arg Ile Leu
            660                 665                 670

Arg Ile Phe Lys Leu Ile Ala Pro Lys Leu Leu Gln Ile Ile Asp Lys
        675                 680                 685

Arg Met Ser His Gln Lys Thr Phe Trp Tyr Gly Ile Leu Lys Gly Tyr
    690                 695                 700

Val Gln Gly Glu Ala Asp Ile Met Thr Ile Ile Asp Gln Ile Thr Ser
705                 710                 715                 720

Ser Lys Gln Ile Lys Gln Met Leu Leu Lys Gln Val Ile Arg Asn Met
                725                 730                 735

Glu His Ala Ile Lys Glu Leu Gly Tyr Leu Glu Tyr Asp His Pro Glu
            740                 745                 750

Ile Ala Val Thr Val Lys Thr Lys Glu Glu Ile Asn Val Met Leu Asn
        755                 760                 765

Met Ala Thr Glu Ile Leu Lys Ala Phe Gly Leu Lys Gly Ile Ile Ser
    770                 775                 780

Lys Thr Glu Gly Ala Gly Ile Asn Lys Leu Ile Met Ala Lys Lys Lys
785                 790                 795                 800

Glu Val Leu Asp Ser Gln Ser Ile Ile Arg Pro Leu Thr Val Glu Glu
                805                 810                 815

Val Leu Tyr His Ile Pro Trp Leu Asp Lys Asn Lys Asp Tyr Ile Asn
            820                 825                 830

Phe Ile Gln Glu Lys Ala Lys Val Val Thr Phe Asp Cys Gly Asn Asp
        835                 840                 845

Ile Phe Glu Glu Gly Asp Glu Pro Lys Gly Ile Tyr Ile Ile Ile Ser
    850                 855                 860
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Gly Met Val Lys Leu Glu Lys Ser Lys Pro Gly Leu Gly Ile Asp Gln
865                 870                 875                 880

Met Val Glu Ser Lys Glu Lys Asp Phe Pro Ile Ile Asp Thr Asp Tyr
                885                 890                 895

Met Leu Ser Gly Glu Ile Ile Gly Glu Ile Asn Cys Leu Thr Asn Glu
            900                 905                 910

Pro Met Lys Tyr Ser Ala Thr Cys Lys Thr Val Val Glu Thr Cys Phe
        915                 920                 925

Ile Pro Lys Thr His Leu Tyr Asp Ala Phe Glu Gln Cys Ser Pro Leu
    930                 935                 940

Ile Lys Gln Lys Met Trp Leu Lys Leu Gly Leu Ala Ile Thr Ala Arg
945                 950                 955                 960

Lys Ile Arg Glu His Leu Ser Tyr Glu Asp Trp Asn Tyr Asn Met Gln
                965                 970                 975

Leu Lys Leu Ser Asn Ile Tyr Val Val Asp Ile Pro Met Ser Thr Lys
            980                 985                 990

Thr Asp Ile Tyr Asp Glu Asn Leu  Ile Tyr Val Ile Leu  Ile His Gly
        995                 1000                1005

Ala Val  Glu Asp Cys Leu Leu  Arg Lys Thr Tyr Arg  Ala Pro Phe
    1010                1015                1020

Leu Ile  Pro Ile Thr Cys His  Gln Ile Gln Ser Ile  Glu Asp Phe
    1025                1030                1035

Thr Lys  Val Val Ile Ile Gln  Thr Pro Ile Asn Met  Lys Thr Phe
    1040                1045                1050

Arg Arg  Asn Ile Arg Lys Phe  Val Pro Lys His Lys  Ser Tyr Leu
    1055                1060                1065

Thr Pro  Gly Leu Ile Gly Ser  Val Gly Thr Leu Glu  Glu Gly Ile
    1070                1075                1080

Gln Glu  Glu Arg Asn Val Lys  Glu Asp Gly Ala His  Ser Ala Ala
    1085                1090                1095

Thr Ala  Arg Ser Pro Gln Pro  Cys Ser Leu Leu Gly  Thr Lys Phe
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1100 1105 1110

Asn Cys Lys Glu Ser Pro Arg Ile Asn Leu Arg Lys Val Arg Lys
1115 1120 1125

Glu

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<220>
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<400> 189
tttgaaccgg cacttgg 17

<210> 190
<211> 23
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<400> 190
tcaaatgcag tagtaaagaa aac 23

<210> 191
<211> 2898
<212> DNA
<213> Homo sapiens

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ccgtctgtgg tgcgtgaccg cgtgtgtgtt gtgggggcgg ggaaaattca tacaaaagaa 120

aaaaatatag cacatctctt ggaaatgaaa tacttcaagt ttaatatctc tcttgctaat 180

gcagaattta tcagccaaga cagctggctg gcctgggtgg ggtttgttaa agttgtcaag 240

tataaggcct actgtaagag ataccaagtg acttttagaa gacagtgtga gggtaaaact 300

gattactatg cttggaaaca cttagtggta caggataaaa ataagtctaa cacacacaaa 360

tacagaatga ttatttgtgt gataaataca gataccattt gtgagatggc ttatgcccat 420

atagaatggg acatgatagt ctgtgcagct tatgcacacg aacttccaaa atacggtgta 480

aaggttggcc tgacaaatga tgctgcagca tgttgtactg gcctgctgct ggcatgcagg 540

cttctcagta ggtttggcat ggacaagatc tataaaggcc aagtggaggt aaccagagat 600

gaatacaacg tgggaagcac tgatggtcag ccaggtgcct ttacctgctg tttggatgca 660

ggccttgcca gaaccaccac tgacaataaa gtttttgggg ctctgagagt gctgtggatg 720

gaggtttctc tatccctcac agtgcctaac gattccctga gtaaagggaa gcctggcccc 780

aggaaggagc agctgcctgc aagagggagc ctgagccgtg gagtcctggg agcctttgag 840

gtgggcagcc agggcgtgga ggcagcagca agcccaaacg gtcaatacgg gcccagctgg 900

ggcctggcgg cggagggcac ggagggagct aggccacagg caccaaagcg ggatttgtcc 960

tatagcagga ctgactctca cagagactgt tctcctgtct gtcacaacat gtccctgagg 1020

ggtcaccttg tccccaagaa gccctcaaag gagaagcagg gacagcagaa actggacagc 1080

aagttttatg agagctgggc cacagccttg ctcacagcta tattcccggt gcttggcatc 1140

ttggtgcttg ttgaatcttt gctgatgaat gacccaatgc gtgaatgcat cctcagcacc 1200

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cggagcagga ccagggctga tcctgcagac gtgctgcccc ctggtgcatt tgagaagact 1380

cgcatgcatg cactgccccc gcctcttggt ttgactttag atgacggtga agtgatcacc 1440

acaagattgc tcactgatgc ttctgtgcaa aaagtcgtgg tccggatatc tgaatcctcc 1500

tcctgcctcc acaatgggct gctatccggt aacggctgtg aggtccatta ccgcagggcg 1560

aggctcttcc aggacgctca gatgcctgct cagagcccag cttatcgggg ggatctgcga 1620

gctcctgtca acgccctgag aattcagaac cggagtcagc tcagcccagg tggaaagatc 1680

aagtggcggc agcacaggca gctggaaggt acccacagaa agaaatcgag cactatgttc 1740

agaaagatcc actccatctt taactccagc ccacagagaa agacggcggc cgagagcccc 1800

ttctacgaag gagccagccc cgcagtgaag ctgattcgaa gcagttccat gtatgtggtc 1860

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caggactgcc tgcagtacct gcaggagctg ctggccttgc gcaaaaaata tctcagcagc 2040

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aagggaggga aaaagactcc tgtccggtct actcccaaag aaataaagaa agcaacccca 2160

aagaaatact cgcagttcag tgctgatgtg gccgaggcca ttgccttctt tgactccatc 2220

attgcagagc tggatacaga gagacgaccc cgggctgctg aggccagcct gccaaatgaa 2280

gatgtggact ttgacgtggc caccagctcc agggagcaca gcttgcattc taactggatc 2340

ctgcgggcac cgcgcagaca ctccgaggat atcgctgccc acactgtgca tactgtagac 2400

ggccagtttc gaaggagcac cgagcacagg accgtgggca ctcagaggag actcgagagg 2460

caccccattt atttgcccaa ggctgtggaa ggggccttca acacctggaa atttaagccc 2520

aaagcctgca aaaaagacct ggggagctcc agacagatcc ttttcaactt ctcaggagaa 2580

gatatggagt gggatgcaga gctctttgcg ttggagcccc agttgtctcc tggggaggac 2640

tactatgaga cagagaaccc caaaggacag tggctgcttc gagaaagact ttgggagcgg 2700

acgactgggt ccctgagaag ctgtccgctt tcagcgcagc atgaggtatt tggtagagtt 2760

gaaaatgcca attgtaacac agtcaaccca ctcagcacac tgcctgctgg tgccgtgcca 2820

gtgccaaaca gacctgtggc ttcccagggg acaggtctca ggacactctc agagcttgag 2880

tttctctgcg tgggctga 2898

<210> 192
<211> 965
<212> PRT
<213> Homo sapiens

<400> 192

Met Trp Val Arg Cys Ala Leu Leu Val Ala Arg Asp Cys Gly Cys Ala
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Glu Arg Val Cys Pro Ser Val Val Arg Asp Arg Val Cys Val Val Gly
20 25 30

Ala Gly Lys Ile His Thr Lys Glu Lys Asn Ile Ala His Leu Leu Glu
35 40 45

Met Lys Tyr Phe Lys Phe Asn Ile Ser Leu Ala Asn Ala Glu Phe Ile
50 55 60

Ser Gln Asp Ser Trp Leu Ala Trp Val Gly Phe Val Lys Val Val Lys
65 70 75 80

Tyr Lys Ala Tyr Cys Lys Arg Tyr Gln Val Thr Phe Arg Arg Gln Cys
85 90 95

Glu Gly Lys Thr Asp Tyr Tyr Ala Trp Lys His Leu Val Val Gln Asp
100 105 110

Lys Asn Lys Ser Asn Thr His Lys Tyr Arg Met Ile Ile Cys Val Ile
115 120 125

Asn Thr Asp Thr Ile Cys Glu Met Ala Tyr Ala His Ile Glu Trp Asp
130 135 140

Met Ile Val Cys Ala Ala Tyr Ala His Glu Leu Pro Lys Tyr Gly Val
145 150 155 160

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Lys Val Gly Leu Thr Asn Asp Ala Ala Ala Cys Cys Thr Gly Leu Leu
                165                 170                 175

Leu Ala Cys Arg Leu Leu Ser Arg Phe Gly Met Asp Lys Ile Tyr Lys
            180                 185                 190

Gly Gln Val Glu Val Thr Arg Asp Glu Tyr Asn Val Gly Ser Thr Asp
        195                 200                 205

Gly Gln Pro Gly Ala Phe Thr Cys Cys Leu Asp Ala Gly Leu Ala Arg
    210                 215                 220

Thr Thr Thr Asp Asn Lys Val Phe Gly Ala Leu Arg Val Leu Trp Met
225                 230                 235                 240

Glu Val Ser Leu Ser Leu Thr Val Pro Asn Asp Ser Leu Ser Lys Gly
                245                 250                 255

Lys Pro Gly Pro Arg Lys Glu Gln Leu Pro Ala Arg Gly Ser Leu Ser
            260                 265                 270

Arg Gly Val Leu Gly Ala Phe Glu Val Gly Ser Gln Gly Val Glu Ala
        275                 280                 285

Ala Ala Ser Pro Asn Gly Gln Tyr Gly Pro Ser Trp Gly Leu Ala Ala
    290                 295                 300

Glu Gly Thr Glu Gly Ala Arg Pro Gln Ala Pro Lys Arg Asp Leu Ser
305                 310                 315                 320

Tyr Ser Arg Thr Asp Ser His Arg Asp Cys Ser Pro Val Cys His Asn
                325                 330                 335

Met Ser Leu Arg Gly His Leu Val Pro Lys Lys Pro Ser Lys Glu Lys
            340                 345                 350

Gln Gly Gln Gln Lys Leu Asp Ser Lys Phe Tyr Glu Ser Trp Ala Thr
        355                 360                 365

Ala Leu Leu Thr Ala Ile Phe Pro Val Leu Gly Ile Leu Val Leu Val
    370                 375                 380

Glu Ser Leu Leu Met Asn Asp Pro Met Arg Glu Cys Ile Leu Ser Thr
385                 390                 395                 400

Ser Gly Phe Ser Gly Pro Arg Ala Arg Leu Leu Gly Val Leu Ala Leu
                405                 410                 415
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Gly Gly Leu Pro Leu His Leu Gly Ala Pro Val Ile Val Met Ala Trp
            420                 425                 430

Ile Val Leu Ala Leu Leu Phe Thr Arg Ser Arg Thr Arg Ala Asp Pro
        435                 440                 445

Ala Asp Val Leu Pro Pro Gly Ala Phe Glu Lys Thr Arg Met His Ala
    450                 455                 460

Leu Pro Pro Pro Leu Gly Leu Thr Leu Asp Asp Gly Glu Val Ile Thr
465                 470                 475                 480

Thr Arg Leu Leu Thr Asp Ala Ser Val Gln Lys Val Val Val Arg Ile
                485                 490                 495

Ser Glu Ser Ser Ser Cys Leu His Asn Gly Leu Leu Ser Gly Asn Gly
            500                 505                 510

Cys Glu Val His Tyr Arg Arg Ala Arg Leu Phe Gln Asp Ala Gln Met
        515                 520                 525

Pro Ala Gln Ser Pro Ala Tyr Arg Gly Asp Leu Arg Ala Pro Val Asn
    530                 535                 540

Ala Leu Arg Ile Gln Asn Arg Ser Gln Leu Ser Pro Gly Gly Lys Ile
545                 550                 555                 560

Lys Trp Arg Gln His Arg Gln Leu Glu Gly Thr His Arg Lys Lys Ser
                565                 570                 575

Ser Thr Met Phe Arg Lys Ile His Ser Ile Phe Asn Ser Ser Pro Gln
            580                 585                 590

Arg Lys Thr Ala Ala Glu Ser Pro Phe Tyr Glu Gly Ala Ser Pro Ala
        595                 600                 605

Val Lys Leu Ile Arg Ser Ser Ser Met Tyr Val Val Gly Asp His Gly
    610                 615                 620

Glu Lys Phe Ser Glu Ser Leu Lys Lys Tyr Lys Ser Thr Ser Ser Met
625                 630                 635                 640

Asp Thr Ser Leu Tyr Tyr Leu Arg Gln Glu Glu Asp Arg Ala Trp Met
                645                 650                 655

Tyr Ser Arg Thr Gln Asp Cys Leu Gln Tyr Leu Gln Glu Leu Leu Ala
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660 665 670

Leu Arg Lys Lys Tyr Leu Ser Ser Phe Ser Asp Leu Lys Pro His Arg
675 680 685

Thr Gln Gly Ile Ser Ser Thr Ser Ser Lys Ser Ser Lys Gly Gly Lys
690 695 700

Lys Thr Pro Val Arg Ser Thr Pro Lys Glu Ile Lys Lys Ala Thr Pro
705 710 715 720

Lys Lys Tyr Ser Gln Phe Ser Ala Asp Val Ala Glu Ala Ile Ala Phe
725 730 735

Phe Asp Ser Ile Ile Ala Glu Leu Asp Thr Glu Arg Arg Pro Arg Ala
740 745 750

Ala Glu Ala Ser Leu Pro Asn Glu Asp Val Asp Phe Asp Val Ala Thr
755 760 765

Ser Ser Arg Glu His Ser Leu His Ser Asn Trp Ile Leu Arg Ala Pro
770 775 780

Arg Arg His Ser Glu Asp Ile Ala Ala His Thr Val His Thr Val Asp
785 790 795 800

Gly Gln Phe Arg Arg Ser Thr Glu His Arg Thr Val Gly Thr Gln Arg
805 810 815

Arg Leu Glu Arg His Pro Ile Tyr Leu Pro Lys Ala Val Glu Gly Ala
820 825 830

Phe Asn Thr Trp Lys Phe Lys Pro Lys Ala Cys Lys Lys Asp Leu Gly
835 840 845

Ser Ser Arg Gln Ile Leu Phe Asn Phe Ser Gly Glu Asp Met Glu Trp
850 855 860

Asp Ala Glu Leu Phe Ala Leu Glu Pro Gln Leu Ser Pro Gly Glu Asp
865 870 875 880

Tyr Tyr Glu Thr Glu Asn Pro Lys Gly Gln Trp Leu Leu Arg Glu Arg
885 890 895

Leu Trp Glu Arg Thr Thr Gly Ser Leu Arg Ser Cys Pro Leu Ser Ala
900 905 910

Gln His Glu Val Phe Gly Arg Val Glu Asn Ala Asn Cys Asn Thr Val
915 920 925

Asn Pro Leu Ser Thr Leu Pro Ala Gly Ala Val Pro Val Pro Asn Arg
930 935 940

Pro Val Ala Ser Gln Gly Thr Gly Leu Arg Thr Leu Ser Glu Leu Glu
945 950 955 960

Phe Leu Cys Val Gly
965

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<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 193
cgagaggcac cccatttatt tg 22

<210> 194
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 194
ttctctgtct catagtagtc ctcccc 26

<210> 195
<211> 1363
<212> DNA
<213> Homo sapiens

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catcccctct tggagcacta aggaccttcc ctgtgttggg aaaactgtct ggctgtacct 120

ccaagcctgg ccaaaccctg tgtttgaagg agatgccctg actctgcgat gtcagggatg 180

gaagaataca ccactgtctc aggtgaagtt ctacagagat ggaaaattcc ttcatttctc 240

taaggaaaac cagactctgt ccatgggagc agcaacagtg cagagccgtg gccagtacag 300

ctgctctggg caggtgatgt atattccaca gacattcaca caaacttcag agactgccat 360

ggttcaagtc caagagctgt ttccacctcc tgtgctgagt gccatcccct ctcctgagcc 420

ccgagagggt agcctggtga ccctgagatg tcagacaaag ctgcaccccc tgaggtcagc 480

cttgaggctc cttttctcct tccacaagga cggccacacc ttgcaggaca ggggccctca 540

cccagaactc tgcatcccgg gagccaagga gggagactct gggctttact ggtgtgaggt 600

ggcccctgag ggtggccagg tccagaagca gagcccccag ctggaggtca gagtgcaggc 660

tcctgtatcc cgtcctgtgc tcactctgca ccacgggcct gctgaccctg ctgtggggga 720

catggtgcag ctcctctgtg aggcacagag gggctcccct ccgatcctgt attccttcta 780

ccttgatgag aagattgtgg ggaaccactc agctccctgt ggtggaacca cctccctcct 840

cttcccagtg aagtcagaac aggatgctgg gaactactcc tgcgaggctg agaacagtgt 900

ctccagagag aggagtgagc ccaagaagct gtctctgaag ggttctcaag tcttgttcac 960

tcccgccagc aactggctgg ttccttggct tcctgcgagc ctgcttggcc tgatggttat 1020

tgctgctgca cttctggttt atgtgagatc ctggagaaaa gctgggcccc ttccatccca 1080

gataccaccc acagctccag gtggagagca gtgcccacta tatgccaacg tgcatcacca 1140

gaaagggaaa gatgaaggtg ttgtctactc tgtggtgcat agaacctcaa agaggagtga 1200

agccaggtct gctgagttca ccgtggggag aaagcacaaa gcttcaccca aattccaccc 1260

caccctggat ctccacacca agcggctcag ggttaatggt cgagttcagg aagcttatgt 1320

ggccttggtc aacacctgct ccctcacccc cagcctgaag tga 1363

<210> 196
<211> 450
<212> PRT
<213> Homo sapiens

<400> 196

Met Leu Leu Trp Thr Ala Val Leu Leu Phe Gly Lys Ser Thr Ser Met
1 5 10 15

Gly Ile Pro Ser Trp Ser Thr Lys Asp Leu Pro Cys Val Gly Lys Thr
20 25 30

Val Trp Leu Tyr Leu Gln Ala Trp Pro Asn Pro Val Phe Glu Gly Asp
35 40 45

Ala Leu Thr Leu Arg Cys Gln Gly Trp Lys Asn Thr Pro Leu Ser Gln
50 55 60

Val Lys Phe Tyr Arg Asp Gly Lys Phe Leu His Phe Ser Lys Glu Asn
65 70 75 80

Gln Thr Leu Ser Met Gly Ala Ala Thr Val Gln Ser Arg Gly Gln Tyr
85 90 95

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Ser Cys Ser Gly Gln Val Met Tyr Ile Pro Gln Thr Phe Thr Gln Thr
            100                 105                 110

Ser Glu Thr Ala Met Val Gln Val Gln Glu Leu Phe Pro Pro Pro Val
        115                 120                 125

Leu Ser Ala Ile Pro Ser Pro Glu Pro Arg Glu Gly Ser Leu Val Thr
    130                 135                 140

Leu Arg Cys Gln Thr Lys Leu His Pro Leu Arg Ser Ala Leu Arg Leu
145                 150                 155                 160

Leu Phe Ser Phe His Lys Asp Gly His Thr Leu Gln Asp Arg Gly Pro
                165                 170                 175

His Pro Glu Leu Cys Ile Pro Gly Ala Lys Glu Gly Asp Ser Gly Leu
            180                 185                 190

Tyr Trp Cys Glu Val Ala Pro Glu Gly Gly Gln Val Gln Lys Gln Ser
        195                 200                 205

Pro Gln Leu Glu Val Arg Val Gln Ala Pro Val Ser Arg Pro Val Leu
    210                 215                 220

Thr Leu His His Gly Pro Ala Asp Pro Ala Val Gly Asp Met Val Gln
225                 230                 235                 240

Leu Leu Cys Glu Ala Gln Arg Gly Ser Pro Pro Ile Leu Tyr Ser Phe
                245                 250                 255

Tyr Leu Asp Glu Lys Ile Val Gly Asn His Ser Ala Pro Cys Gly Gly
            260                 265                 270

Thr Thr Ser Leu Leu Phe Pro Val Lys Ser Glu Gln Asp Ala Gly Asn
        275                 280                 285

Tyr Ser Cys Glu Ala Glu Asn Ser Val Ser Arg Glu Arg Ser Glu Pro
    290                 295                 300

Lys Lys Leu Ser Leu Lys Gly Ser Gln Val Leu Phe Thr Pro Ala Ser
305                 310                 315                 320

Asn Trp Leu Val Pro Trp Leu Pro Ala Ser Leu Leu Gly Leu Met Val
                325                 330                 335

Ile Ala Ala Ala Leu Leu Val Tyr Val Arg Ser Trp Arg Lys Ala Gly
            340                 345                 350
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Pro Leu Pro Ser Gln Ile Pro Pro Thr Ala Pro Gly Gly Glu Gln Cys
355 360 365

Pro Leu Tyr Ala Asn Val His His Gln Lys Gly Lys Asp Glu Gly Val
370 375 380

Val Tyr Ser Val Val His Arg Thr Ser Lys Arg Ser Glu Ala Arg Ser
385 390 395 400

Ala Glu Phe Thr Val Gly Arg Lys His Lys Ala Ser Pro Lys Phe His
405 410 415

Pro Thr Leu Asp Leu His Thr Lys Arg Leu Arg Val Asn Gly Arg Val
420 425 430

Gln Glu Ala Tyr Val Ala Leu Val Asn Thr Cys Ser Leu Thr Pro Ser
435 440 445

Leu Lys
450

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<211> 19
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<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 197
gtcagggatg gaagaatac 19

<210> 198
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<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 198
acaggaggtg gaaacagc 18

<210> 199
<211> 534
<212> DNA
<213> Homo sapiens

<400> 199
acaattgtgt cttcttccag atgtcatcgc tataaggagt ggggctttca tcacctcctt 60

gacgtaggat gtgtacatgg ctctccaggt cagagttgct ccaagcaagg ttgttttgca 120

gaagtttctt ctatgtgtca ttcttttcta cactgtgtac tatgtgtccc tgagcatggg 180

ctgcgtgatg tttgaggtgc atgagttgaa tgtcctggct ccatttgatt tcaaaacaaa 240

tccctcatgg ctcaacataa actataaagt tcttttagtt tcaacagagg tcacctactt 300

tgtttgtgga ttgtttttg ttccagttgt ggaagaatgg gtttgggatt atgctatttc 360

agtcactatt cttcatgttg ccatcacttc aactgttatg ttggaattcc ccttgacatc 420

acattggtgg gctgctttag gtatatcaaa attgcttgtt tagattctct aatgcacaga 480

aataatgtta aatagaataa ctgtggaaat atattttatt ttctcataga tttt 534

<210> 200
<211> 128
<212> PRT
<213> Homo sapiens

<400> 200

Met Ala Leu Gln Val Arg Val Ala Pro Ser Lys Val Val Leu Gln Lys
1 5 10 15

Phe Leu Leu Cys Val Ile Leu Phe Tyr Thr Val Tyr Tyr Val Ser Leu
20 25 30

Ser Met Gly Cys Val Met Phe Glu Val His Glu Leu Asn Val Leu Ala
35 40 45

Pro Phe Asp Phe Lys Thr Asn Pro Ser Trp Leu Asn Ile Asn Tyr Lys
50 55 60

Val Leu Leu Val Ser Thr Glu Val Thr Tyr Phe Val Cys Gly Leu Phe
65 70 75 80

Phe Val Pro Val Val Glu Glu Trp Val Trp Asp Tyr Ala Ile Ser Val
85 90 95

Thr Ile Leu His Val Ala Ile Thr Ser Thr Val Met Leu Glu Phe Pro
100 105 110

Leu Thr Ser His Trp Trp Ala Ala Leu Gly Ile Ser Lys Leu Leu Val
115 120 125

<210> 201
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 201
tcaaacatca cgcagcccat 20

<210> 202
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 202
tggggctttc atcacctcct tg 22

<210> 203
<211> 615
<212> DNA
<213> Homo sapiens

<400> 203
ggggatgtga tgtcaggctt gattgtgggc atattattgg tgccccagtc cattgcttat 60

tccctgctgg ctggccaaga acctgtctat ggtctgtaca catcttttt tgccagcatc 120

atttattttc tcttgggtac ctcccgtcac atctctgtgg gcatttttgg agtactgtgc 180

cttatgattg gtgagacagt tgaccgagaa ctacagaaag ctggctatga caatgcccat 240

agtgctcctt ccttaggaat ggtttcaaat gggagcacat tattaaatca tacatcagac 300

aggatatgtg acaaaagttg ctatgcaatt atggttggca gcactgtaac ctttatagct 360

ggagtttatc agtgattgtt ttgttaatgt ggaagcaaca ttttctatga ttaatctgct 420

gttacctgtt ttgactgagc tactacaaaa agaaaaatca ctgaattgct atgggtttct 480

gaaatatcca aaaaattaac ctgaagcagg gggaaaaatg acatcacacc attagcaggt 540

attgtgtgaa acttctaaaa atgaaactga catttatctg acttattagg aataaatact 600

ctctaatgaa ctctc 615

<210> 204
<211> 121
<212> PRT
<213> Homo sapiens

<400> 204

Met Ser Gly Leu Ile Val Gly Ile Leu Leu Val Pro Gln Ser Ile Ala
1 5 10 15

Tyr Ser Leu Leu Ala Gly Gln Glu Pro Val Tyr Gly Leu Tyr Thr Ser
20 25 30

Phe Phe Ala Ser Ile Ile Tyr Phe Leu Leu Gly Thr Ser Arg His Ile
35 40 45

Ser Val Gly Ile Phe Gly Val Leu Cys Leu Met Ile Gly Glu Thr Val
50 55 60

Asp Arg Glu Leu Gln Lys Ala Gly Tyr Asp Asn Ala His Ser Ala Pro
65 70 75 80

Ser Leu Gly Met Val Ser Asn Gly Ser Thr Leu Leu Asn His Thr Ser
85 90 95

Asp Arg Ile Cys Asp Lys Ser Cys Tyr Ala Ile Met Val Gly Ser Thr
100 105 110

Val Thr Phe Ile Ala Gly Val Tyr Gln
115 120

<210> 205
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 205
taaatcatac atcagacagg 20

<210> 206
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 206
aaaacaggta acagcagatt 20

<210> 207
<211> 513
<212> DNA
<213> Homo sapiens

<400> 207
atggcggcgg ccgctctcgc gagaattcgg cccgtcgggc tccaagcccg gcgcctggcg 60

tcggagggaa agactcgagc cgaaagcccc atctctgacc ctagcaactc ataccccttct 120

ggcttccctt tagcaaagcg cctggacgtc atcccctctt cagatacccc aggcctcgtc 180

ctggccactg gcttgactat tgcaggagag cctgataaga tgggacacgg ctccaccttg 240

cattcagcaa gtcgttatcc tgcaactacg atgcaccagg aagaggatgt ggtgaggcca 300

gcttttccat atgcagttag gcatcgaagg gaagatctgc tgtacctaag tggggtgggc 360

atttcatttt tagggaccgt ctttgttaaa ataatttggg acctcataaa gcctccagcc 420

attcctgatc aggacatagc ttacaacagc agcctggtgc ccataacctg gacagcctgg 480

agtgaagtca cactcccaga cttgatgttc taa 513

<210> 208
<211> 170
<212> PRT
<213> Homo sapiens

<400> 208

Met Ala Ala Ala Ala Leu Ala Arg Ile Arg Pro Val Gly Leu Gln Ala
1 5 10 15

Arg Arg Leu Ala Ser Glu Gly Lys Thr Arg Ala Glu Ser Pro Ile Ser
20 25 30

Asp Pro Ser Asn Ser Tyr Pro Ser Gly Phe Pro Leu Ala Lys Arg Leu
35 40 45

Asp Val Ile Pro Ser Ser Asp Thr Pro Gly Leu Val Leu Ala Thr Gly
50 55 60

Leu Thr Ile Ala Gly Glu Pro Asp Lys Met Gly His Gly Ser Thr Leu
65 70 75 80

His Ser Ala Ser Arg Tyr Pro Ala Thr Thr Met His Gln Glu Glu Asp
85 90 95

Val Val Arg Pro Ala Phe Pro Tyr Ala Val Arg His Arg Arg Glu Asp
100 105 110

Leu Leu Tyr Leu Ser Gly Val Gly Ile Ser Phe Leu Gly Thr Val Phe
115 120 125

Val Lys Ile Ile Trp Asp Leu Ile Lys Pro Pro Ala Ile Pro Asp Gln
130 135 140

Asp Ile Ala Tyr Asn Ser Ser Leu Val Pro Ile Thr Trp Thr Ala Trp
145 150 155 160

Ser Glu Val Thr Leu Pro Asp Leu Met Phe
165 170

<210> 209
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 209
tgagccctag atatacttgg 20

<210> 210
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 210
cagtcagcct ccatttct 18

<210> 211
<211> 508
<212> DNA
<213> Homo sapiens

<400> 211
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cttacatgct ggagtcaccc tcagtttgtc aaagtgttca cactgtgaga ggctcacaga 120

aatggaggct gactgaagga agagcagatt cacatctttc atcccttctt tatgctcatg 180

cttctaattt ttgttcccat gttttcttgc ccctcctctt cttagcattt attttgtctg 240

tttctctttc ccctcttctg gctccctctc catctctcct gagcacagaa atgcggctac 300

tgtatttaat ccacagtggc cccctctggc cccctctttg tgtctcctga gcacaggccc 360

tggccccctc tccatctctc ctgacctcct gatccgccca cctcggccag ttattgctgt 420

tttataagga aaatgttttc tagtaccaca cttgtctccc tggaagggat agaagaagga 480

gggaaggaag tagggaggca gggaagag 508

<210> 212
<211> 97
<212> PRT
<213> Homo sapiens

<400> 212

Met Pro Tyr Met Leu Glu Ser Pro Ser Val Cys Gln Ser Val His Thr
1 5 10 15

Val Arg Gly Ser Gln Lys Trp Arg Leu Thr Glu Gly Arg Ala Asp Ser
20 25 30

His Leu Ser Ser Leu Leu Tyr Ala His Ala Ser Asn Phe Cys Ser His
35 40 45

Val Phe Leu Pro Leu Leu Phe Leu Ala Phe Ile Leu Ser Val Ser Leu
50 55 60

Ser Pro Leu Leu Ala Pro Ser Pro Ser Leu Leu Ser Thr Glu Met Arg
65 70 75 80

Leu Leu Tyr Leu Ile His Ser Gly Pro Leu Trp Pro Pro Leu Cys Val
85 90 95

Ser

<210> 213
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 213
ctgtatttaa tccacagtgg ccccc 25

<210> 214
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 214
tccctacttc cttccctcct tcttcta 27

<210> 215
<211> 1321
<212> DNA
<213> Homo sapiens

<400> 215
cagtgcccag gcaagcccag gagttgacat ttctctgccc agccatgggc ctcaccctgc 60

tcttgctgct gctcctggga ctagaaggtc agggcatagt tggcagcctc cctgaggtgc 120

tgcaggcacc cgtgggaagc tccattctgg tgcagtgcca ctacaggctc caggatgtca 180

aagctcagaa ggtgtggtgc cggttcttgc cggaggggtg ccagcccctg gtgtcctcag 240

ctgtggatcg cagagctcca gcgggcaggc gtacgtttct cacagacctg ggtgggggcc 300

tgctgcaggt ggaaatggtt accctgcagg aagaggatgc tggcgagtat ggctgcatgg 360

tggatggggc caggggggccc cagattttgc acagagtctc tctgaacata ctgcccccag 420

aggaagaaga agagacccat aagattggca gtctggctga gaacgcattc tcagaccctg 480

caggcagtgc caacccttg gaacccagcc aggatgagaa gagcatcccc ttgatctggg 540

gtgctgtgct cctggtaggt ctgctggtgg cagcggtggt gctgtttgct gtgatggcca 600

agaggaaaca agggaacagg cttggtgtct gtggccgatt cctgagcagc agagtttcag 660

gcatgaatcc ctcctcagtg gtccaccacg tcagtgactc tggaccggct gctgaattgc 720

ctttggatgt accacacatt aggcttgact caccaccttc atttgacaat accacctaca 780

ccagcctacc tcttgattcc ccatcaggaa aaccttcact cccagctcca tcctcattgc 840

cccctctacc tcctaaggtc ctggtctgct ccaagcctgt gacatatgcc acagtaatct 900

tcccgggagg gaacaagggt ggagggacct cgtgtgggcc agcccagaat ccacctaaca 960

atcagactcc atccagctaa gctgctcatc acactttaaa ctcatgagga ccatccctag 1020

gggttctgtg catccatcca gccagctcat gccctaggat ccttaggata tctgagcaac 1080

cagggacttt aagatctaat ccaatgtcct aactttacta gggaaagtga cgctcagaca 1140

tgactgagat gtcttgggga agacctccct gcacccaact cccccactgg ttcttctacc 1200

attacacact gggctaaata aaccctaata atgatgtgca aactcttaat ggctgaatgg 1260

gaaaggaaac tgcccaagtt tgactaattg cttggcctgt gaatggaaaa gactctggtc 1320

t 1321

<210> 216
<211> 311
<212> PRT
<213> Homo sapiens

<400> 216

Met Gly Leu Thr Leu Leu Leu Leu Leu Leu Leu Gly Leu Glu Gly Gln
1 5 10 15

Gly Ile Val Gly Ser Leu Pro Glu Val Leu Gln Ala Pro Val Gly Ser
20 25 30

Ser Ile Leu Val Gln Cys His Tyr Arg Leu Gln Asp Val Lys Ala Gln
35 40 45

Lys Val Trp Cys Arg Phe Leu Pro Glu Gly Cys Gln Pro Leu Val Ser
50 55 60

Ser Ala Val Asp Arg Arg Ala Pro Ala Gly Arg Arg Thr Phe Leu Thr
65 70 75 80

Asp Leu Gly Gly Gly Leu Leu Gln Val Glu Met Val Thr Leu Gln Glu
85 90 95

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Glu Asp Ala Gly Glu Tyr Gly Cys Met Val Asp Gly Ala Arg Gly Pro
            100                 105                 110

Gln Ile Leu His Arg Val Ser Leu Asn Ile Leu Pro Pro Glu Glu Glu
        115                 120                 125

Glu Glu Thr His Lys Ile Gly Ser Leu Ala Glu Asn Ala Phe Ser Asp
    130                 135                 140

Pro Ala Gly Ser Ala Asn Pro Leu Glu Pro Ser Gln Asp Glu Lys Ser
145                 150                 155                 160

Ile Pro Leu Ile Trp Gly Ala Val Leu Leu Val Gly Leu Leu Val Ala
                165                 170                 175

Ala Val Val Leu Phe Ala Val Met Ala Lys Arg Lys Gln Gly Asn Arg
            180                 185                 190

Leu Gly Val Cys Gly Arg Phe Leu Ser Ser Arg Val Ser Gly Met Asn
        195                 200                 205

Pro Ser Ser Val Val His His Val Ser Asp Ser Gly Pro Ala Ala Glu
    210                 215                 220

Leu Pro Leu Asp Val Pro His Ile Arg Leu Asp Ser Pro Pro Ser Phe
225                 230                 235                 240

Asp Asn Thr Thr Tyr Thr Ser Leu Pro Leu Asp Ser Pro Ser Gly Lys
                245                 250                 255

Pro Ser Leu Pro Ala Pro Ser Ser Leu Pro Pro Leu Pro Pro Lys Val
            260                 265                 270

Leu Val Cys Ser Lys Pro Val Thr Tyr Ala Thr Val Ile Phe Pro Gly
        275                 280                 285

Gly Asn Lys Gly Gly Gly Thr Ser Cys Gly Pro Ala Gln Asn Pro Pro
    290                 295                 300

Asn Asn Gln Thr Pro Ser Ser
305                 310
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<210> 217
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 217
aggaagaaga agagaccc 18

<210> 218
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 218
catcacagca aacagcac 18

<210> 219
<211> 3874
<212> DNA
<213> Homo sapiens

<400> 219
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gaaccctgag ctcggcgcgc cgagagtccc agcagggcaa gggggcgcgg cgtcctggtc 120

ctcgagcttg ggagacagat gcgcatgggc gtgggggcat gcggacctaa gctcgggtga 180

agctctcggg aagggcaaga ctgcggcgac gagatgcgag cagaggagcc ctgcgccccc 240

ggggccccca gcgccctggg agcccagcgc acgccgggcc ccgagctgcg cctgtccagc 300

cagctgctgc ccgagctctg taccttcgtg gtgcgcgtgc tgttctacct ggggcctgtc 360

tacctagctg gctacctggg gctcagcata acctggttgc tgctcggcgc cctgctgtgg 420

atgtggtggc gcaggaaccg ccgcgggaag cttgggcgcc tggccgccgc cttcgaattc 480

cttgacaatg aacgcgagtt catcagccgc gagctgcggg gccagcacct gccagcctgg 540

atccacttcc cggacgtgga gcgggtcgag tgggccaaca agatcatctc tcagacctgg 600

ccctacctaa gcatgatcat ggaaagcaag ttccgggaga aacttgagcc caagatccga 660

gagaagagca tccacctgag gacctttacc tttaccaagc tctactttgg acagaagtgt 720

cccagggtca acggtgtcaa ggcacacact aatacgtgca accgaagacg tgtgactgtg 780

gacctgcaga tctgctacat cggggactgt gagatcagtg tggagctgca gaagattcag 840

gctggtgtga acgggatcca gttgcagggc accctgcggg tcatcctgga gcccctccta 900

gtggacaagc cctttgtggg agccgtgact gtgttcttcc ttcagaagca gcacctacag 960

atcaactgga ctggcctgac caacctgctg gatgcgccgg gaatcaatga tgtgtcagac 1020

agcttactgg aggacctcat tgccacccac ctggtgctgc ccaaccgtgt gactgtgcct 1080

gtgaagaagg ggctggatct gaccaacctg cgcttccctc tgccctgtgg ggtgatcaga 1140

gtgcacttgc tggaggcaga gcagctggcc cagaaggaca actttctggg gctccgaggc 1200

aagtcagatc cctacgccaa ggtgagcatc ggcctacagc atttccggag taggaccatc 1260

tacaggaacc tgaaccccac ctggaacgaa gtgtttgagt tcatggtgta cgaagtccct 1320

ggacaggacc tggaggtaga cctgtatgat gaggataccg acagggatga cttcctgggc 1380

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gaccaagaag ttctgactga ggaccatggt ggcctttcca ctgccattct cgtggtcttc 1560

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tctgaaggtt tgatggaaga agggctcttg aaacagagtt aagaggtttt taagccaggc 1860

gggctgggaa gcttgaagtg caccttgagc aggttctcct ggcagcgttt aaagtcagcc 1920

ccttgtatgt aagagaggac actgaggccc cacaaggcct catctcctta aggctagtgc 1980

ctgaggtcac tgtatagggg gatgtgggag gataaatcct caagtccctt gactttccct 2040

gcaaaagggt ctttatattt gctacacagt acccagagca gcctatctac acaggacatt 2100

aataatggtg tactttaaaa aatatatgtt tcatttaatc ttcacaaaag atctgtagag 2160

taagcaaaga gaggcaaaaa caatgtcttg tccaagatct catgaccaac aagtggtgga 2220

gctgggatct tttagggccc tgagccctgc ctggagagca gcacagctca tcagtcccca 2280

aagccccctg gctctgggca tttgacagac tagctcatac agatcataat tgcctctact 2340

ctgagtcact atcttccctg acagaagaca aggaccaggt ctggcctgat cccattctag 2400

ttttcagaat aggaccagat gcccatagaa gcacagtaca gactgaagta aacccaaact 2460

tggctggggc tcagatacta gtagtggagt ggtggggctt ggttatcctc ttgttttgtg 2520

actggaccac tgcccaggtg cttgatgatg accaggagtg tgctctggga atgctggagg 2580

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accactcagg cctggacagc ctcatctcca tgaggctggt gcttgcagtt cctgcaagtg 2700

gaggaacgag agctggggag cccatacaca ggacctgaag ccctaaagaa aggccctctg 2760

ctcatcaaga aagtggctac caaccagggt cccaaagccc aacctcagga agaaggccct 2820

acagatttgc catgtccccc agaccctgct tctgatacta aggacgtatc caggagtacc 2880

acaaccacca ccagtgctac caccgttgcc actgagccca catcccaaga gacaggccca 2940

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ccagccacca tcttcctgac tgtcccaggt ccccactctc cagggcccat caagtcaccc 3060

agacccatga aatgccctgc ctccccattc gcatggccgc ccaagaggct ggctcccagc 3120

atgtcctcgc tcaactcctt ggcctcttct tgctttgacc tggcagatat cagcctcaac 3180

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ctggatggaa aagtagatat gaacttacat ttctgtgcaa gttgtttttt cacaaaatat 3300

cttcctaaga ggcagcatgg tgtggtagaa agaacacagg acaagggaga gagagccaaa 3360

caggctgttt atggctctag ctgcgtactg actataaaat agatgctgga ctctggttga 3420

ggtggggacc tcaggcgacg gcagctgggt gagattcagc tcacagtgcg ctatgtgtgt 3480

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agtggagctg atccctacgt ccgtgtctac ttgttgccag aaaggaagtg ggcatgtcgt 3600

aagaagactt cagtgaagcg gaagaccttg gaacccctgt ttgatgagac atttgaattt 3660

tttgttccca tggaagaagt aaagaagagg tcactagatg ttgcagtgaa aaatagtagg 3720

ccacttggct cacacagaag aaaggagtta ggaaaagtac tgattgactt atcaaaagaa 3780

gatctgatta agggcttttc acaatggtaa gtgtgccctt tcattttatc actgttatcc 3840

tgctattcaa gacagttttc ccttttcagt actg 3874

<210> 220
<211> 501
<212> PRT
<213> Homo sapiens

<400> 220

Met Arg Ala Glu Glu Pro Cys Ala Pro Gly Ala Pro Ser Ala Leu Gly
1 5 10 15

Ala Gln Arg Thr Pro Gly Pro Glu Leu Arg Leu Ser Ser Gln Leu Leu
20 25 30

Pro Glu Leu Cys Thr Phe Val Val Arg Val Leu Phe Tyr Leu Gly Pro
35 40 45

Val Tyr Leu Ala Gly Tyr Leu Gly Leu Ser Ile Thr Trp Leu Leu Leu
50 55 60

Gly Ala Leu Leu Trp Met Trp Trp Arg Arg Asn Arg Arg Gly Lys Leu
65 70 75 80

Gly Arg Leu Ala Ala Ala Phe Glu Phe Leu Asp Asn Glu Arg Glu Phe
85 90 95

```
Ile Ser Arg Glu Leu Arg Gly Gln His Leu Pro Ala Trp Ile His Phe
            100                 105                 110

Pro Asp Val Glu Arg Val Glu Trp Ala Asn Lys Ile Ile Ser Gln Thr
        115                 120                 125

Trp Pro Tyr Leu Ser Met Ile Met Glu Ser Lys Phe Arg Glu Lys Leu
    130                 135                 140

Glu Pro Lys Ile Arg Glu Lys Ser Ile His Leu Arg Thr Phe Thr Phe
145                 150                 155                 160

Thr Lys Leu Tyr Phe Gly Gln Lys Cys Pro Arg Val Asn Gly Val Lys
                165                 170                 175

Ala His Thr Asn Thr Cys Asn Arg Arg Arg Val Thr Val Asp Leu Gln
            180                 185                 190

Ile Cys Tyr Ile Gly Asp Cys Glu Ile Ser Val Glu Leu Gln Lys Ile
        195                 200                 205

Gln Ala Gly Val Asn Gly Ile Gln Leu Gln Gly Thr Leu Arg Val Ile
    210                 215                 220

Leu Glu Pro Leu Leu Val Asp Lys Pro Phe Val Gly Ala Val Thr Val
225                 230                 235                 240

Phe Phe Leu Gln Lys Gln His Leu Gln Ile Asn Trp Thr Gly Leu Thr
                245                 250                 255

Asn Leu Leu Asp Ala Pro Gly Ile Asn Asp Val Ser Asp Ser Leu Leu
            260                 265                 270

Glu Asp Leu Ile Ala Thr His Leu Val Leu Pro Asn Arg Val Thr Val
        275                 280                 285

Pro Val Lys Lys Gly Leu Asp Leu Thr Asn Leu Arg Phe Pro Leu Pro
    290                 295                 300

Cys Gly Val Ile Arg Val His Leu Leu Glu Ala Glu Gln Leu Ala Gln
305                 310                 315                 320

Lys Asp Asn Phe Leu Gly Leu Arg Gly Lys Ser Asp Pro Tyr Ala Lys
                325                 330                 335

Val Ser Ile Gly Leu Gln His Phe Arg Ser Arg Thr Ile Tyr Arg Asn
            340                 345                 350
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Leu Asn Pro Thr Trp Asn Glu Val Phe Glu Phe Met Val Tyr Glu Val
        355                 360                 365

Pro Gly Gln Asp Leu Glu Val Asp Leu Tyr Asp Glu Asp Thr Asp Arg
    370                 375                 380

Asp Asp Phe Leu Gly Ser Leu Gln Ile Cys Leu Gly Asp Val Met Thr
385                 390                 395                 400

Asn Arg Val Val Asp Glu Trp Phe Val Leu Asn Asp Thr Thr Ser Gly
                405                 410                 415

Arg Leu His Leu Arg Leu Glu Trp Leu Ser Leu Leu Thr Asp Gln Glu
            420                 425                 430

Val Leu Thr Glu Asp His Gly Gly Leu Ser Thr Ala Ile Leu Val Val
        435                 440                 445

Phe Leu Glu Ser Ala Cys Asn Leu Pro Arg Asn Pro Phe Asp Tyr Leu
    450                 455                 460

Asn Gly Glu Tyr Arg Ala Lys Lys Leu Ser Arg Phe Ala Arg Val Lys
465                 470                 475                 480

Gln Gly Gln Gln Arg Pro Phe Phe Leu Cys Gln Thr Ile Cys Arg Gln
                485                 490                 495

Glu Asp Thr Tyr Lys
            500
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<210> 221
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 221
tggggcctgt ctacctagct 20

<210> 222
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 222

tcttgttggc ccactcgac 19

<210> 223
<211> 1020
<212> DNA
<213> Homo sapiens

<400> 223
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ataaatcact tcaatttccc aatgaatttt atattgttta tttttatacc tggagttttt 120

tccttaaaaa gtagcacttt gaagcctact attgaagcat tgcctaatgt gctaccttta 180

aatgaagatg ttaataagca ggaagaaaag aatgaagatc atactcccaa ttatgctcct 240

gctaatgaga aaaatggcaa ttattataaa gatataaaac aatatgtgtt cacaacacaa 300

aatccaaatg gcactgagtc tgaaatatct gtgagagcca caactgacct gaattttgct 360

ctaaaaaacg ataaaactgt caatgcaact acatatgaaa aatccaccat tgaagaagaa 420

acaactacta gcgaaccctc tcataaaaat attcaaagat caaccccaaa cgtgcctgca 480

ttttggacaa tgttagctaa agctataaat ggaacagcag tggtcatgga tgataaagat 540

caattatttc acccaattcc agagtctgat gtgaatgcta cacagggaga aaatcagcca 600

gatctagagg atctgaagat caaaataatg ctgggaatct cgttgatgac cctcctcctc 660

tttgtggtcc tcttggcatt ctgtagtgct acactgtaca aactgaggca tctgagttat 720

aaaagttgtg agagtcagta ctctgtcaac ccagagctgg ccacgatgtc ttactttcat 780

ccatcagaag gtgtttcaga tacatccttt tccaagagtg cagagagcag cacatttttg 840

ggtaccactt cttcagatat gagaagatca ggcacaagaa catcagaatc taagataatg 900

acggatatca tttccatagg ctcagataat gagatgcatg aaaacgatga gtcggttacc 960

cggtgaagaa atcaaggaac ccggtgaaga aatcttattg atgaataaat aactttaatt 1020

<210> 224
<211> 294
<212> PRT
<213> Homo sapiens

<400> 224

Met Asn Phe Ile Leu Phe Ile Phe Ile Pro Gly Val Phe Ser Leu Lys
1 5 10 15

Ser Ser Thr Leu Lys Pro Thr Ile Glu Ala Leu Pro Asn Val Leu Pro
20 25 30

Leu Asn Glu Asp Val Asn Lys Gln Glu Glu Lys Asn Glu Asp His Thr
35 40 45

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Pro Asn Tyr Ala Pro Ala Asn Glu Lys Asn Gly Asn Tyr Tyr Lys Asp
    50                  55                  60

Ile Lys Gln Tyr Val Phe Thr Thr Gln Asn Pro Asn Gly Thr Glu Ser
65                  70                  75                  80

Glu Ile Ser Val Arg Ala Thr Thr Asp Leu Asn Phe Ala Leu Lys Asn
                85                  90                  95

Asp Lys Thr Val Asn Ala Thr Thr Tyr Glu Lys Ser Thr Ile Glu Glu
            100                 105                 110

Glu Thr Thr Thr Ser Glu Pro Ser His Lys Asn Ile Gln Arg Ser Thr
        115                 120                 125

Pro Asn Val Pro Ala Phe Trp Thr Met Leu Ala Lys Ala Ile Asn Gly
    130                 135                 140

Thr Ala Val Val Met Asp Asp Lys Asp Gln Leu Phe His Pro Ile Pro
145                 150                 155                 160

Glu Ser Asp Val Asn Ala Thr Gln Gly Glu Asn Gln Pro Asp Leu Glu
                165                 170                 175

Asp Leu Lys Ile Lys Ile Met Leu Gly Ile Ser Leu Met Thr Leu Leu
            180                 185                 190

Leu Phe Val Val Leu Leu Ala Phe Cys Ser Ala Thr Leu Tyr Lys Leu
        195                 200                 205

Arg His Leu Ser Tyr Lys Ser Cys Glu Ser Gln Tyr Ser Val Asn Pro
    210                 215                 220

Glu Leu Ala Thr Met Ser Tyr Phe His Pro Ser Glu Gly Val Ser Asp
225                 230                 235                 240

Thr Ser Phe Ser Lys Ser Ala Glu Ser Ser Thr Phe Leu Gly Thr Thr
                245                 250                 255

Ser Ser Asp Met Arg Arg Ser Gly Thr Arg Thr Ser Glu Ser Lys Ile
            260                 265                 270

Met Thr Asp Ile Ile Ser Ile Gly Ser Asp Asn Glu Met His Glu Asn
        275                 280                 285

Asp Glu Ser Val Thr Arg
    290
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<210> 225
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 225
tgaatgctac acagggagaa aatc 24

<210> 226
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 226
tgaaagtaag acatcgtggc c 21

<210> 227
<211> 309
<212> DNA
<213> Homo sapiens

<400> 227
atgaccacag ccacccctct gggggatacc accttcttct cactgaacat gaccaccagg 60

ggagaagact tcctgtataa gagttctgga gccattgttg ctgccgttgt ggtggttgtc 120

atcatcatct tcaccgtggt tctgatcctg ctgaagatgt acaacaggaa aatgaggacg 180

aggcgggaac tagagcccaa gggccccaag ccaaccgccc cttctgccgt gggcccaaac 240

agcaacggca gccaacaccc agcaactgtg accttcagtc ctgttgacgt ccaggtggag 300

acgcgatga 309

<210> 228
<211> 102
<212> PRT
<213> Homo sapiens

<400> 228

Met Thr Thr Ala Thr Pro Leu Gly Asp Thr Thr Phe Phe Ser Leu Asn
1 5 10 15

Met Thr Thr Arg Gly Glu Asp Phe Leu Tyr Lys Ser Ser Gly Ala Ile
20 25 30

Val Ala Ala Val Val Val Val Val Ile Ile Ile Phe Thr Val Val Leu
35 40 45

Ile Leu Leu Lys Met Tyr Asn Arg Lys Met Arg Thr Arg Arg Glu Leu
50 55 60

Glu Pro Lys Gly Pro Lys Pro Thr Ala Pro Ser Ala Val Gly Pro Asn
65 70 75 80

Ser Asn Gly Ser Gln His Pro Ala Thr Val Thr Phe Ser Pro Val Asp
85 90 95

Val Gln Val Glu Thr Arg
100

<210> 229
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 229
ggggatacca ccttcttct 19

<210> 230
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 230
agttgctggg tgttggct 18

<210> 231
<211> 2510
<212> DNA
<213> Homo sapiens

<400> 231
gacttttaa taatagtcgt tctgactgat gtgaaatgga gtctctttgt ggttctgatt 60

tgcatctctg atgatgcatg atgttgacca gtttttaata tgtttgttga ctgcttgtat 120

gtcttctttt aagaagtgtc tgttcatatc ctttgccctt tcgcttctat gcaccaataa 180

cacccaggct gagagtcaaa ccaagaacac aatcctgact acagtagcca taaagaaaat 240

gaaatacctg ggaatacacc taatcaaaaa catgaaagca ctctctagag ggagaactac 300

aaaacattgc tgaaagaaat cagagatgat tctctgaaaa agaagtcaga ttagaaatga 360

ttctctgaaa aagaaatcat ctctgatttc tttcagcagt gtgtttttg tttgtttgtt 420

tgttttgaga cagagtcttg ctctgtcgcc aaggctggag ggcaatggca tgatttcagc 480

tcactacaac ctcctgctcc tgggttcgag cgattctcct acctcagcct cccgagtagc 540

tgggattaca ggaggctgag aaaatgttag aaattggggg agacaagttt cccttagaga 600

gcaggaagtt actaagtagt cctggaaaga acatcagttg cagatgtgac ccctctgaga 660

ttaatatatc tgatgaaatg cctaaaacta cagtttggaa agctctcagt atgaattctg 720

gaaatgcaaa ggaaaagagt ctcttcaact aagagtcttt gctgggatgg aagatttggg 780

ccgtgtggtg cctcagggaa gttctggtta cagagaaaat ggcgagtctc tcagagaaga 840

agcaagacca agtctggccc tgtccttggt catctcaaag ccatgccgaa gcattcagtt 900

attcttggtg tgcattggaa ggcatccagc tatccccata ccagcagcca gtcaccagat 960

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ctctgctggc ctgccaagcc atatggattc attctgccac tgaggagtcc ttcagtgagg 1140

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tcaacagtaa gtgaggatga gcagtgtctc ttggttttca ttgaggatag agtaagagat 1560

tgagtttaga ttgcaacaga aggaattagt ttagatacca ggaagaactt cctagcctga 1620

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<210> 232
<211> 164
<212> PRT
<213> Homo sapiens

<400> 232

Met Gln Arg Lys Arg Val Ser Ser Thr Lys Ser Leu Cys Trp Asp Gly
1 5 10 15

Arg Phe Gly Pro Cys Gly Ala Ser Gly Lys Phe Trp Leu Gln Arg Lys
20 25 30

Trp Arg Val Ser Gln Arg Arg Ser Lys Thr Lys Ser Gly Pro Val Leu
35 40 45

Gly His Leu Lys Ala Met Pro Lys His Ser Val Ile Leu Gly Val His
50 55 60

Trp Lys Ala Ser Ser Tyr Pro His Thr Ser Ser Gln Ser Pro Asp Val
65 70 75 80

Asn Val Glu Ala Glu Asp His Leu Leu Leu Val Leu Leu Leu Phe Leu
85 90 95

Leu Phe Leu Phe Arg Thr Ala Thr Ile Glu Asp Leu Ala Ser His Phe
100 105 110

Pro Asp Val Phe Ser Glu Ile Leu Cys Trp Pro Ala Lys Pro Tyr Gly
115 120 125

Phe Ile Leu Pro Leu Arg Ser Pro Ser Val Arg Ser Leu Phe Leu Lys
130 135 140

Asp Arg Val Gly Ser Arg Arg Gly Thr Glu Arg Thr Ser Ser Leu Ala
145 150 155 160

Leu Gln Cys Ser

<210> 233
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 233
gaggctgaga aaatgttaga 20

<210> 234
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 234
tccatcccag caaagact 18

<210> 235
<211> 1977
<212> DNA
<213> Homo sapiens

<400> 235
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cttggaagac tggagacaga aggcagagtc tcaggctctg aaggtataag gagtgtgagt 120

tcctgtgaga aacactcatt tgattgtgaa aagacttgaa ttctatgcta agcagggttc 180

caagtagcta aatgaatgat ctcagcaagt ctctcttgct gctgctgcta ctcgtttaca 240

tttattgatt acttacgatg attcaggtac tgttgtaagt gctttacatg ctgttatacg 300

agactcttgg gagaaatcac tttaatgaag cttgagacac atggcattgc catgcaatga 360

tttttccccc ctcttcacgg gatcagaggg aactaataga atgtgacaat gattctttag 420

cagggactgc tgaggcttct ggttcctttt taagatctgc agtgaaagaa gatgagaaac 480

atggatatgc ccttcttttg gtccccctct tcctttattt gatctctact tccttctata 540

aatatattag ggctacattg tccctttgta tttcaaacaa ggcaaaaaga ggttgtaatt 600

acactttact gcaatcctca gtttctccag ggaacaggaa tgcaaaggct ttgaaggcct 660

ctctatttgc tgacatggtc agctgggtgc catgggccaa gtccttctgt tgccctcctc 720

tgtcaccaag taagctaggt cctttctgag gctcaggttt gctgtgatga tgatcacttt 780

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tggtatcttg gaatttccat gtcattacag tctacagaat gaaagagtaa cctgtcccag 960

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taaaataata aatgtatgta ggaatacgtg tgttgaaaga tgtacatcaa tttgctaaca 1860

atggttatct ctgacgtggt gggatttgag atgtgttttt ctttttggtt gtatttttct 1920

ctattgtttg acttaacaca gaacatgttt ggttacaaca ataaagttat tgaagac 1977

<210> 236
<211> 130
<212> PRT
<213> Homo sapiens

<400> 236

Met Ile Phe Pro Pro Ser Ser Arg Asp Gln Arg Glu Leu Ile Glu Cys
1 5 10 15

Asp Asn Asp Ser Leu Ala Gly Thr Ala Glu Ala Ser Gly Ser Phe Leu
20 25 30

Arg Ser Ala Val Lys Glu Asp Glu Lys His Gly Tyr Ala Leu Leu Leu
35 40 45

Val Pro Leu Phe Leu Tyr Leu Ile Ser Thr Ser Phe Tyr Lys Tyr Ile
50 55 60

Arg Ala Thr Leu Ser Leu Cys Ile Ser Asn Lys Ala Lys Arg Gly Cys
65 70 75 80

Asn Tyr Thr Leu Leu Gln Ser Ser Val Ser Pro Gly Asn Arg Asn Ala
85 90 95

Lys Ala Leu Lys Ala Ser Leu Phe Ala Asp Met Val Ser Trp Val Pro
100 105 110

Trp Ala Lys Ser Phe Cys Cys Pro Pro Leu Ser Pro Ser Lys Leu Gly
115 120 125

Pro Phe
130

<210> 237
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 237
atgattcttt agcaggga 18

<210> 238
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 238
ctctttttgc cttgtttg 18

<210> 239
<211> 1293
<212> DNA
<213> Homo sapiens

<400> 239
aggccgaggg gttcggcgac gcggagggag ggagagtctg ggccgcgcgg gagccgcagg 60

gcgccctagc cttcgcagaa acgatggcgg aggaagaagg accacctgta gagctgcgcc 120

aaagaaaaaa gccaaagtct tcagaaaata aggaatctgc caaagaagag aaaatcagtg 180

acattccaat tcctgaaaga gctccaaaac atgtattatt tcaacgcttt gcaaagattt 240

tcattggctg tcttgcagcg gttactagtg gtatgatgta tgctctctac ttatcagcat 300

accatgaacg gaaattctgg ttttccaaca ggcaggagct tgaacgggaa atcacgtttc 360

agggtgacag tgccatttat tactcctatt ataaagatat gttaaaggca ccttcatttg 420

aaagaggtgt ttacgaactg acacacaata acaaaactgt atctctgaag actataaatg 480

cagtgcagca aatgtctctg tatccggaac ttattgctag cattttatat caagccactg 540

gtagcaatga gattattgag ccagtgtatt tctatattgg cattgttttt ggattgcaag 600

gaatatatgt tactgcttta tttgttacaa gttggcttat gagtggaaca tggctagcag 660

gaatgcttac tgttgcgtgg ttcgttatta acagttgcac agacccctgg tacagtgtgg 720

gaggtgacaa cacaggatat taataccagg aggcaggaat cattgggacc gtcttggagg 780

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atatttgaag aggaaaagat actttctcat gtaaacataa tggttttaaa gaataagact 900

ctcttatgct acttaaacaa aagaataaga ctctctttag agatcttagt gagaattgta 960

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gacaattgaa atgttcttaa tagctaagtt ttaaaaaatg cgtttgtttg ctttttgttt 1140

atattttatt ggtatgtatc ttgtactgca aaatacattt taatgccatg aaagaatatg 1200

ctgtctcttt attcatcagc tttatagctt ttatttatat atgacttctt agaaaagtat 1260

aaaaagatat taaagtcatt ccattatatt atg 1293

<210> 240
<211> 219
<212> PRT
<213> Homo sapiens

<400> 240

Met Ala Glu Glu Glu Gly Pro Pro Val Glu Leu Arg Gln Arg Lys Lys
1 5 10 15

Pro Lys Ser Ser Glu Asn Lys Glu Ser Ala Lys Glu Glu Lys Ile Ser
20 25 30

Asp Ile Pro Ile Pro Glu Arg Ala Pro Lys His Val Leu Phe Gln Arg
35 40 45

Phe Ala Lys Ile Phe Ile Gly Cys Leu Ala Ala Val Thr Ser Gly Met
50 55 60

Met Tyr Ala Leu Tyr Leu Ser Ala Tyr His Glu Arg Lys Phe Trp Phe
65 70 75 80

Ser Asn Arg Gln Glu Leu Glu Arg Glu Ile Thr Phe Gln Gly Asp Ser
85 90 95

Ala Ile Tyr Tyr Ser Tyr Tyr Lys Asp Met Leu Lys Ala Pro Ser Phe
100 105 110

Glu Arg Gly Val Tyr Glu Leu Thr His Asn Asn Lys Thr Val Ser Leu
115 120 125

Lys Thr Ile Asn Ala Val Gln Gln Met Ser Leu Tyr Pro Glu Leu Ile
130 135 140

Ala Ser Ile Leu Tyr Gln Ala Thr Gly Ser Asn Glu Ile Ile Glu Pro
145 150 155 160

Val Tyr Phe Tyr Ile Gly Ile Val Phe Gly Leu Gln Gly Ile Tyr Val
165 170 175

Thr Ala Leu Phe Val Thr Ser Trp Leu Met Ser Gly Thr Trp Leu Ala
180 185 190

Gly Met Leu Thr Val Ala Trp Phe Val Ile Asn Ser Cys Thr Asp Pro
195 200 205

Trp Tyr Ser Val Gly Gly Asp Asn Thr Gly Tyr
210 215

<210> 241
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 241
accgctgcaa gacagccaa 19

<210> 242
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 242
gcagaaacga tggcggagga 20

<210> 243
<211> 1291
<212> DNA
<213> Homo sapiens

<400> 243
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gacagctgca tggaaaacaa aattctgctg ggagtaaatg gaggcctgtg cctgcttata 120

tcattggtag ccatctcacc ctgggtccaa aatcgacagc cacactcggg gctcttacaa 180

tcaggggtca taagctgcta tgtcacctac ctcaccttct cagctctgtc cagcaaacct 240

gcagaagtag ttctagatga acatgggaaa aatgttacaa tctgtgtgcc tgactttggt 300

caagacctgt acagagatga aaacttggtg actatactgg ggaccagcct cttaatcgga 360

tgtatcttgt attcatgttt gacatcaaca acaagatcga gttctgacgc tctgcagggg 420

cgatacgcag ctcctgaatt ggagatagct cgctgttgtt tttgcttcag tcctggtgga 480

gaggacactg aagagcagca gccggggaag gagggaccac gggtcattta tgacgagaag 540

aaaggcaccg tctacatcta ctcctacttc cacttcgtgt tcttcctagc ttccctgtat 600

gtgatgatga ccgtcaccaa ctggttcaac tacgaaagtg ccaacatcga gagcttcttc 660

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tacctgtgta cgctggtcgc tcccctctgc tgccccaccc gggagttctc tgtgtgatga 780

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gaaaaaaaaa aatctcctga ttagcttttt acttttgaaa ttcaaaaaga aactaccagt 960

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gggcacagca tcttttcaca gggataaaaa tatcttgtgg ggccagtcat tctcatcctc 1140

ggaatagaaa aacatgccaa aatcttgagt ccccagcgcc taacagaatc cagacccctc 1200

tcactcactt ccgcctctta gagccttgtc cccaggggc tttgaggaca ggactcagcc 1260

tgcagggccc ctggtattta tagggtccaa g 1291

<210> 244
<211> 257
<212> PRT
<213> Homo sapiens

<400> 244

Met Tyr Ser Ile Ala Thr Gly Gly Leu Val Leu Met Ala Val Phe Tyr
1 5 10 15

Thr Gln Lys Asp Ser Cys Met Glu Asn Lys Ile Leu Leu Gly Val Asn
20 25 30

Gly Gly Leu Cys Leu Leu Ile Ser Leu Val Ala Ile Ser Pro Trp Val
35 40 45

Gln Asn Arg Gln Pro His Ser Gly Leu Leu Gln Ser Gly Val Ile Ser
50 55 60

Cys Tyr Val Thr Tyr Leu Thr Phe Ser Ala Leu Ser Ser Lys Pro Ala
65 70 75 80

Glu Val Val Leu Asp Glu His Gly Lys Asn Val Thr Ile Cys Val Pro
85 90 95

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Asp Phe Gly Gln Asp Leu Tyr Arg Asp Glu Asn Leu Val Thr Ile Leu
            100                 105                 110

Gly Thr Ser Leu Leu Ile Gly Cys Ile Leu Tyr Ser Cys Leu Thr Ser
        115                 120                 125

Thr Thr Arg Ser Ser Ser Asp Ala Leu Gln Gly Arg Tyr Ala Ala Pro
    130                 135                 140

Glu Leu Glu Ile Ala Arg Cys Cys Phe Cys Phe Ser Pro Gly Gly Glu
145                 150                 155                 160

Asp Thr Glu Glu Gln Gln Pro Gly Lys Glu Gly Pro Arg Val Ile Tyr
                165                 170                 175

Asp Glu Lys Lys Gly Thr Val Tyr Ile Tyr Ser Tyr Phe His Phe Val
            180                 185                 190

Phe Phe Leu Ala Ser Leu Tyr Val Met Met Thr Val Thr Asn Trp Phe
        195                 200                 205

Asn Tyr Glu Ser Ala Asn Ile Glu Ser Phe Phe Ser Gly Ser Trp Ser
    210                 215                 220

Ile Phe Trp Val Lys Met Ala Ser Cys Trp Ile Cys Val Leu Leu Tyr
225                 230                 235                 240

Leu Cys Thr Leu Val Ala Pro Leu Cys Cys Pro Thr Arg Glu Phe Ser
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Val
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<210> 245
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 245
agtcaggcac acagattg 18

<210> 246
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 246
ttctgctggg agtaaatg 18

<210> 247
<211> 2412
<212> DNA
<213> Homo sapiens

<400> 247
gaacccaggc atcctgggct ccagctgaaa ccattgcatg tggctttccc catccctggc 60

cccgtgactc agtccctctg aagggagcag ccctcttttt tggcaatcac cagggaggtg 120

gggggaggag gaggggagct aggtggtgac atcacagtcg aaggttataa aagcttccag 180

ccaaacggca ttgaagttga agatacaacc tgacagcaca gcctgagatc ttggggatcc 240

ctcagcctaa cacccacaga cgtcagctgg tggattcccg ctgcatcaag gcctacccac 300

tgtctccatg ctgggctctc cctgccttct gtggctcctg gccgtgacct tcttggttcc 360

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gccctgcaag gagctacaga gggtcgggcc ggcggcctgc ctgtgcccag gactctccag 540

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ccgcgcagtg gtccactggt gtgccccctt ctccccggtc ctccactact ggctgctgct 660

ttgggacggc agcgaggctg cgcagaaggg gcccccgctg aacgctacgg tccgcagagc 720

cgaactgaag gggctgaagc caggggggcat ttatgtcgtt tgcgtagtgg ccgctaacga 780

ggccggggca agccgcgtgc cccaggctgg aggagagggc ctcgaggggg ccgacatccc 840

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acgacctgac ttagtaatgc gaacctatag tagcagctac tccagaggct gaaatgggag 1440

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agatcgagac catcctggct aacacggtga aaccccgtct ctactaaaaa tacaaaaatt 1980

agccgggcat ggtggtgggt acctgtagtc ccagctactc cggaggctga ggcaggagaa 2040

tggcgtgaac ccgggaggcg gatcttgcag tgagcggaga ttgcaccact gcactccagc 2100

ctgggtgaca gagcaagact ccctctcaaa agaaaaagaa aaaagatgta aaaaccattc 2160

ttagtttgtg ggccttacaa atcaggccac tggcccattg cttgtagtta gttgatccat 2220

gtcatgcacc ctaaaaatgg ctctgtcact gtgagtggct tcagtaggat tttgagaata 2280

agtttatatt cttgctaggt aaaacaaaac aaaaacgaca gtaataccaa ggaatctccc 2340

ccccctttta ccctccattt gtgtttattg catatccact ataacaacat taaaggacct 2400

ttaaaaggaa gt 2412

<210> 248
<211> 238
<212> PRT
<213> Homo sapiens

<400> 248

Met Leu Gly Ser Pro Cys Leu Leu Trp Leu Leu Ala Val Thr Phe Leu
1 5 10 15

Val Pro Arg Ala Gln Pro Leu Ala Pro Gln Asp Phe Glu Glu Glu Glu
20 25 30

Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala Val Pro Cys
35 40 45

Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys Lys Glu Leu Gln
50 55 60

Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly Leu Ser Ser Pro Ala
65 70 75 80

Gln Pro Pro Asp Pro Pro Arg Met Gly Glu Val Arg Ile Ala Ala Glu
85 90 95

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Glu Gly Arg Ala Val Val His Trp Cys Ala Pro Phe Ser Pro Val Leu
            100                 105                 110

His Tyr Trp Leu Leu Leu Trp Asp Gly Ser Glu Ala Ala Gln Lys Gly
        115                 120                 125

Pro Pro Leu Asn Ala Thr Val Arg Arg Ala Glu Leu Lys Gly Leu Lys
    130                 135                 140

Pro Gly Gly Ile Tyr Val Val Cys Val Val Ala Ala Asn Glu Ala Gly
145                 150                 155                 160

Ala Ser Arg Val Pro Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp
                165                 170                 175

Ile Pro Ala Phe Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro
            180                 185                 190

Arg Thr Leu Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu
        195                 200                 205

Leu Ser Cys Ala Ala Leu Val Trp His Phe Cys Leu Arg Asp Arg Trp
    210                 215                 220

Gly Cys Pro Arg Arg Ala Ala Ala Arg Ala Ala Gly Ala Leu
225                 230                 235
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<210> 249
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 249
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<210> 250
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 250
gccgtctcag tctcatct 18

<210> 251

<211> 1024
<212> DNA
<213> Homo sapiens

<400> 251
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gacgaggaga gctgcgggga caacgcctgt ggctgggtcc ggaggtgcgg gtgcggcgcg 120

ggacaagcgg gcagcatgct cagggcggtc gggagcctac tgcgccttgg ccgcgggcta 180

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atcctgctgt ggacagggcg tttcaaatcg atggaggaga tcccgcctcg gatcccgcca 420

gaaatgatag acaccgcaag aaacaaagct cgagtgaaag cttgttacat aatgattgga 480

ctcacaatta tcgcctgctt tgctgtgata gtgtcagcca aaagggctgt agaacgacat 540

gaatccttaa caagttggaa cttggcaaag aaagctaagt ggcgtgaaga agctgcattg 600

gctgcacagg ctaaagctaa atgatattct aagtgacaaa gtgttcacct gaataccatc 660

cctgtcatca gcaacagtag aagatgggaa aaatagaata tttaccaaaa tatctgccat 720

ggttttattt tggtaacaag aagcacaatg tctttttttat ttttattttt tagtaaactt 780

ttactgaagt ataccatgca ttcaaaaagt ggacaaaact gtatacagtc tgatagatat 840

ttatgtcgtg aacacctgtg taaccactgc caaagtgaag atgtagaata ttggcaacac 900

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atta 1024

<210> 252
<211> 162
<212> PRT
<213> Homo sapiens

<400> 252

Met Leu Arg Ala Val Gly Ser Leu Leu Arg Leu Gly Arg Gly Leu Thr
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Val Arg Cys Gly Pro Gly Ala Pro Leu Glu Ala Thr Arg Arg Pro Ala
20 25 30

Pro Ala Leu Pro Pro Arg Gly Leu Pro Cys Tyr Ser Ser Gly Gly Ala
35 40 45

Pro Ser Asn Ser Gly Pro Gln Gly His Gly Glu Ile His Arg Val Pro

50 55 60

Thr Gln Arg Arg Pro Ser Gln Phe Asp Lys Lys Ile Leu Leu Trp Thr
65 70 75 80

Gly Arg Phe Lys Ser Met Glu Glu Ile Pro Pro Arg Ile Pro Pro Glu
85 90 95

Met Ile Asp Thr Ala Arg Asn Lys Ala Arg Val Lys Ala Cys Tyr Ile
100 105 110

Met Ile Gly Leu Thr Ile Ile Ala Cys Phe Ala Val Ile Val Ser Ala
115 120 125

Lys Arg Ala Val Glu Arg His Glu Ser Leu Thr Ser Trp Asn Leu Ala
130 135 140

Lys Lys Ala Lys Trp Arg Glu Glu Ala Ala Leu Ala Ala Gln Ala Lys
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Ala Lys

<210> 253
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<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 253
attatcgcct gctttgctg 19

<210> 254
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 254
ttcccatctt ctactgttgc tg 22

<210> 255
<211> 852
<212> DNA
<213> Homo sapiens

<400> 255
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gcagccaccc ctccatgtgg gccacagggg aggagcttag gaagccgcct tggcaaggtt 720

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<210> 256
<211> 110
<212> PRT
<213> Homo sapiens

<400> 256

Met Trp Ser Leu Trp Ile Trp Val Asp Gln His Gln Ala Arg Leu Ile
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Pro Ser Pro Gln Val Leu Leu Leu Leu Leu Arg Glu Ala Pro Ser Thr
20 25 30

Ala Ala Ala Val Ala Gly Trp Leu Val Val Ala Ser Met Ala Leu Leu
35 40 45

Gln Leu His Ala Val Gly Gly Val Ala Leu Thr Ser Ser His Pro Ser
50 55 60

Met Trp Ala Thr Gly Glu Glu Leu Arg Lys Pro Pro Trp Gln Gly Ser
65 70 75 80

Ala Gly Ser Ala Ser Gly Val Glu Glu Leu Thr Gly Lys His Ser Cys
85 90 95

Pro Gly Pro Glu Glu Pro Ala Thr Val Gln Lys Ala Pro Ala
100 105 110

<210> 257
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 257
ttgctgttcc cattcata 18

<210> 258
<211> 19
<212> DNA
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<220>
<223> Oligonucleotide

<400> 258
gataaagtct ggttcctcc 19

<210> 259
<211> 4231
<212> DNA
<213> Homo sapiens

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tatgaagatg agattgtgct ggattattaa gcaccctaaa tgccatgaca ggtgtccttc 3300

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aaaaaaaaca tgagctttga agtgcacagg g 4231

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<211> 359
<212> PRT
<213> Homo sapiens

<400> 260

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Leu Arg Asn Pro Ala Ile Ala Val Ala Leu Pro Val Val Tyr Ser Leu
20 25 30

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Val Ala Ala Val Ser Ile Pro Gly Asn Leu Phe Ser Leu Trp Val Leu
        35                  40                  45

Cys Arg Arg Met Gly Pro Arg Ser Pro Ser Val Ile Phe Met Ile Asn
    50                  55                  60

Leu Ser Val Thr Asp Leu Met Leu Ala Ser Val Leu Pro Phe Gln Ile
65                  70                  75                  80

Tyr Tyr His Cys Asn Arg His His Trp Val Phe Gly Val Leu Leu Cys
                85                  90                  95

Asn Val Val Thr Val Ala Phe Tyr Ala Asn Met Tyr Ser Ser Ile Leu
            100                 105                 110

Thr Met Thr Cys Ile Ser Val Glu Arg Phe Leu Gly Val Leu Tyr Pro
        115                 120                 125

Leu Ser Ser Lys Arg Trp Arg Arg Arg Arg Tyr Ala Val Ala Ala Cys
    130                 135                 140

Ala Gly Thr Trp Leu Leu Leu Leu Thr Ala Leu Ser Pro Leu Ala Arg
145                 150                 155                 160

Thr Asp Leu Thr Tyr Pro Val His Ala Leu Gly Ile Ile Thr Cys Phe
                165                 170                 175

Asp Val Leu Lys Trp Thr Met Leu Pro Ser Val Ala Met Trp Ala Val
            180                 185                 190

Phe Leu Phe Thr Ile Phe Ile Leu Leu Phe Leu Ile Pro Phe Val Ile
        195                 200                 205

Thr Val Ala Cys Tyr Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu
    210                 215                 220

Glu Ala His Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala
225                 230                 235                 240

Val Val Leu Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val
                245                 250                 255

Leu Leu Ala His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr
            260                 265                 270

His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu
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275 280 285

Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu
290 295 300

Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr
305 310 315 320

Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu
325 330 335

Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu
340 345 350

Gln Arg Gln Glu Ser Val Phe
355

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<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 261
cctgttacct ggagaccct 19

<210> 262
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 262
accagcgagt acaccacg 18

<210> 263
<211> 717
<212> DNA
<213> Homo sapiens

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ggaagaaact cgcattgtct actggatcaa ggacagacag ctcaccaacc gtgacagcac 120

catactggaa cttcaaaaag ttctgaaaac atgttgtgct cagagcatga aaattttctg 180

ctgtctttgg aactttgtct acaaacagtt agaagatgca gcccaagggc tcaccatggg 240

tggcgatgtt gaagaacatg aagaccttac tgctgatagc accatcttca aatttgtgga 300

agcttataca gagtgggagg tgaagaggtg gtcagacaac aatctgataa tgaaacaaac 360

aaatgtgaag agaagacgct tagatgatgt tggccctgaa ttggaaaagg ctgtctggga 420

gctcggctgc ccacccagca ttcagtgtct gctacctcct gtctgttatg cttgtgtctg 480

gtttttcaa gttttaattt ttttttaat tcttagtttt tgtgggtaca tagtaggtgt 540

atatatttat gggttacatg agatgttttg atacaggcat gcaatatgta ataatcacct 600

catggagaat ggggtaccca tcacatcaag catttatcct ttgtgttaca aacggtccag 660

ttagactctt ttagttatta ttaaaatgta caattaaatt atttttgact atagtca 717

<210> 264
<211> 171
<212> PRT
<213> Homo sapiens

<400> 264

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Thr Asn Arg Asp Ser Thr Ile Leu Glu Leu Gln Lys Val Leu Lys Thr
20 25 30

Cys Cys Ala Gln Ser Met Lys Ile Phe Cys Cys Leu Trp Asn Phe Val
35 40 45

Tyr Lys Gln Leu Glu Asp Ala Ala Gln Gly Leu Thr Met Gly Gly Asp
50 55 60

Val Glu Glu His Glu Asp Leu Thr Ala Asp Ser Thr Ile Phe Lys Phe
65 70 75 80

Val Glu Ala Tyr Thr Glu Trp Glu Val Lys Arg Trp Ser Asp Asn Asn
85 90 95

Leu Ile Met Lys Gln Thr Asn Val Lys Arg Arg Arg Leu Asp Asp Val
100 105 110

Gly Pro Glu Leu Glu Lys Ala Val Trp Glu Leu Gly Cys Pro Pro Ser
115 120 125

Ile Gln Cys Leu Leu Pro Pro Val Cys Tyr Ala Cys Val Trp Phe Phe
130 135 140

Gln Val Leu Ile Phe Phe Leu Ile Leu Ser Phe Cys Gly Tyr Ile Val
145 150 155 160

Gly Val Tyr Ile Tyr Gly Leu His Glu Met Phe
165 170

<210> 265
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<400> 265
ttcaacatcg ccacccat 18

<210> 266
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<212> DNA
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<400> 266
cagcagaggg gaagtggtca 20

<210> 267
<211> 390
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<213> Homo sapiens

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gatctggagg ttggaggttt agctggacag ccccttaaag ttttcactcc acgtaaaaaa 180

ggttctgggg aagtgggtga tgcttctcag tcgcccagca gaagcaatga tggccagcat 240

tcctgcattg gccacagcag agatctctgc tgctacactg ctcagaccct cataatctcc 300

tacacatcaa atggtctttc tcctttagca actccaccct tccaccctat tcctggaaac 360

tgctacgaca gtgttgatta taaaatatag 390

<210> 268
<211> 129
<212> PRT
<213> Homo sapiens

<400> 268

Met Glu Val Ile Leu Pro Asp Lys Pro Gln Val Asp Ala Leu Ala Phe
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Leu Ala Ala Val Thr Met Leu Trp Ile Thr Leu Pro Met Ser Pro Phe
20 25 30

Ala Glu Ala Glu Lys Leu Ala Trp Asp Leu Glu Val Gly Gly Leu Ala
35 40 45

Gly Gln Pro Leu Lys Val Phe Thr Pro Arg Lys Lys Gly Ser Gly Glu
50 55 60

Val Gly Asp Ala Ser Gln Ser Pro Ser Arg Ser Asn Asp Gly Gln His
65 70 75 80

Ser Cys Ile Gly His Ser Arg Asp Leu Cys Cys Tyr Thr Ala Gln Thr
85 90 95

Leu Ile Ile Ser Tyr Thr Ser Asn Gly Leu Ser Pro Leu Ala Thr Pro
100 105 110

Pro Phe His Pro Ile Pro Gly Asn Cys Tyr Asp Ser Val Asp Tyr Lys
115 120 125

Ile

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<211> 2856
<212> DNA
<213> Homo sapiens

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atggccatgg aggtctttgt catcttggca tcagcaggag gcctcatgtc ctcccctcttc 2760

ttttccaaat gctacatcat ccttctccat cctgaaaaga acacaaaaga ccaaatgttt 2820

ggccggcatc atcgcaagtg ggaaaaactg aagtga 2856

<210> 270
<211> 951
<212> PRT
<213> Homo sapiens

<400> 270

Met Ala Lys Arg Asn Leu Ser Thr Val Thr Glu Phe Ile Leu Val Val
1 5 10 15

Phe Thr Asp His Pro Glu Leu Ala Val Pro Leu Phe Leu Val Phe Leu
20 25 30

Ser Phe Tyr Leu Val Thr Phe Leu Gly Asn Gly Gly Met Ile Ile Leu
35 40 45

Ile Gln Val Asp Ala Gln Leu His Thr Pro Val Tyr Phe Phe Leu Ser
50 55 60

His Leu Ala Phe Leu Asp Ala Cys Cys Ala Ser Val Ile Thr Pro Gln
65 70 75 80

Ile Leu Ala Thr Leu Ala Thr Asp Lys Thr Val Ile Ser Tyr Gly Cys
85 90 95

Arg Ala Val Gln Phe Ser Phe Phe Thr Ile Cys Ala Gly Thr Glu Cys
100 105 110

Tyr Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Ser Asn
115 120 125

Pro Leu His Cys Asn Met Thr Met Thr Pro Gly Thr Cys Arg Val Phe
130 135 140

Leu Ala Ser Ala Phe Ile Cys Gly Val Ser Gly Ala Ile Leu His Thr
145 150 155 160

Thr Cys Thr Phe Thr Leu Ser Phe Cys Cys Asp Asn Gln Ile Asn Phe
165 170 175

Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Ser Met
180 185 190

```
Thr Gln Thr Glu Ile Val Ile Leu Leu Cys Ala Lys Cys Met Phe Leu
        195                 200                 205

Ala Asn Val Met Val Ile Leu Ile Cys Tyr Met Leu Ile Ile Arg Ala
    210                 215                 220

Ile Leu Arg Val Lys Ser Ala Gly Gly Leu Leu Ile Ala Ser Ala His
225                 230                 235                 240

Phe Asp Ala Tyr Val Tyr Glu Thr Gly Ile Asn Tyr Asn Thr Val Tyr
                245                 250                 255

Gly Ser Gly Lys Ala Val Gly Trp Ser Trp Arg Ser Leu Arg Glu Thr
            260                 265                 270

Asn His Met Arg Pro Gly Asn Thr Ser Lys His Ser Ala Ala Gln Leu
        275                 280                 285

His Gln Cys Leu Ile Gln Gln Val Gly Arg Trp Pro Leu Gln Ser Met
    290                 295                 300

Pro Phe Pro Val Ser Ala Gly Pro Pro Tyr Lys Ser Val Gln Pro Leu
305                 310                 315                 320

Pro Gly Asp Pro Arg Pro Leu Leu Cys Ile Thr Gly Leu Phe Leu Thr
                325                 330                 335

Leu Lys Met Met Gly Cys Gly Pro Arg Arg Pro Arg Asp Arg Lys Ser
            340                 345                 350

Asp Phe Phe Ile Asn Thr Asp Pro Gly Ala Gly Ser Pro Glu Glu Gln
        355                 360                 365

Arg Cys Gly Trp Glu Gly His Pro Ser His Ser Tyr Thr Leu Gly Leu
    370                 375                 380

Ser Leu Pro Val Asn Phe Gly Leu Lys Cys Pro Trp Trp Thr Leu Ser
385                 390                 395                 400

Gly Pro Pro Ala Thr Cys Gln Arg Pro Asp Leu Gln Thr Pro Ser Pro
                405                 410                 415

Pro Lys Glu Ile Cys Ser Ser Gly Leu Arg Pro Leu Thr His Ser Ala
            420                 425                 430

Gly Pro Asp Arg Ser Gln Val Pro Ala Ala Ser Gly Ala Ala Thr Met
        435                 440                 445
```

```
Leu Thr Lys Gly Leu Pro Asp Ile Thr Val Gly Leu Gln Ile Tyr Asp
    450                 455                 460

Ser Cys Ile Ser Gly Ile Gln Ala Leu Gly Ser Thr Leu Ala Leu Leu
465                 470                 475                 480

Ser Asn Gln Leu Pro Pro Thr Thr Asn Tyr Ala Cys Gly Ser Gln Gln
                485                 490                 495

His Leu Leu Gly Val Val Gly Gly Met Thr Phe Leu Glu Ser Glu Pro
            500                 505                 510

Met Ser Glu Leu Leu Ser Ile Tyr Arg Val Pro Gln Gly Gln Arg Leu
        515                 520                 525

Thr Lys Asn Phe Glu Val Lys Glu Leu Val Cys Thr Tyr Leu Val Gly
    530                 535                 540

Gln Leu Pro Tyr Gly Leu Val Ser Tyr Asp Asn Ser Asn Phe Glu Trp
545                 550                 555                 560

Leu Asp Gln Gln Leu Gln Lys Gln Ile Gly Gly Glu Gly Leu Pro Val
                565                 570                 575

Gly Ala Ala Pro Ser Arg Val Ala Arg Gln Gln Ser Asp Glu Glu Ala
            580                 585                 590

Val Gly Gly Val Gln Gly Tyr Arg Trp Ser Gly Leu Gly Ala Ser Ile
        595                 600                 605

Gln Ser Ala Arg Glu Gly Ala Trp His Arg Thr Gly Leu Glu Asn Met
    610                 615                 620

Thr Thr Ala His Leu Ser Ala Phe Lys Leu Pro Asp Leu Thr Ala Thr
625                 630                 635                 640

Tyr Gln Ala Tyr Leu Ala Ala Lys Ala Leu Trp Val Ala Tyr Gln Asn
                645                 650                 655

Leu Met Ser Cys Ser Glu Arg Glu Gly Pro Phe Leu Gly Gly Thr Tyr
            660                 665                 670

Ala Asn Ala Trp Glu Ala Arg Leu Ser Gln Val Asn Phe Thr Thr Lys
        675                 680                 685

Ala Gln Glu Glu Val Phe Phe Ala Lys Asp Gly Glu Val Leu Thr Thr
```

690 695 700

Phe Asp Ile Lys Asn Ile Tyr Val Leu Pro Asp Leu Ser Gly Gln Thr
705 710 715 720

Ala Ile Val Gly His Phe Asp Phe Arg Ala Pro Ser Gly Lys Glu Leu
725 730 735

Leu Leu Asp Asp Ser Ala Ile Val Trp Ala Glu Gly Pro Leu Lys Ile
740 745 750

Arg Ala Glu Arg Thr Leu Arg Thr Lys Thr Thr Gln His Leu Ser His
755 760 765

Pro Lys Leu Gln Glu Ser Leu Pro Leu Ser Ala Thr Lys Asn Val Leu
770 775 780

Trp Lys Pro Gly Ser Gln Pro Tyr Leu Arg Ser Gln Asn Ala Ala Thr
785 790 795 800

Lys Ala Phe Pro Asp Pro Glu Glu Lys Ser Gln Cys His Gln Phe Leu
805 810 815

Phe Leu Pro Ser Asp Ser Val Ala Cys Gln Lys Cys Ser Asp Asn Gln
820 825 830

Trp Pro Asn Val Gln Lys Gly Glu Cys Ile Pro Lys Thr Leu Asp Phe
835 840 845

Leu Phe Tyr His Lys Pro Leu Asp Thr Ala Leu Ala Val Cys Thr Ala
850 855 860

Leu Leu Phe Leu Leu Ala Leu Ala Ile Leu Gly Ile Phe His Val Val
865 870 875 880

Cys Ser Cys Val Trp Val Ser Phe Ile Pro Ala His Met His Ala His
885 890 895

Ser Lys Asp Thr Met Ala Met Glu Val Phe Val Ile Leu Ala Ser Ala
900 905 910

Gly Gly Leu Met Ser Ser Leu Phe Phe Ser Lys Cys Tyr Ile Ile Leu
915 920 925

Leu His Pro Glu Lys Asn Thr Lys Asp Gln Met Phe Gly Arg His His
930 935 940

```
Arg Lys Trp Glu Lys Leu Lys
945                 950
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<210> 271
<211> 956
<212> DNA
<213> Homo sapiens

<400> 271

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ccacctggtg gcaatggctc agccacacct gacaatggca ccacccctgg ggccgagggc    120

tggcggcagt tgctgggcct actccccgag cacatggcgg agaagctgtg tgaggcctgg    180

gcctttgggc agagccacca gacgggcgtc gtggcactgg gcctactcac ctgcctgctg    240

gcaatgctgc tggctggccg catcaggctc cggaggatcg atgccttctg cacctgcctg    300

tgggccctgc tgctggggct gcacctggct gagcagcacc tgcaggccgc ctcgcctagc    360

tggctagaca cgctcaagtt cagcaccaca tctttgtgct gcctggttgg cttcacggcg    420

gctgtggcca caaggaaggc aacgggccca cggaggttcc ggccccgaag gttcttccca    480

ggagactctg ccggcctttt ccccaccagc cccagcttgg ccatccctca cccgagtgtc    540

ggaggctctc cagcgtctct gttcatcccc agcccgccca gcttcctgcc cctcgccaac    600

caagcagctc ttccggtctc ctcgacggac ctcaccctcc tcatttgcct ggccgcctca    660

gccgggccct ctctctggga accataccct ctctgactcg agcagactcc ggctatctgt    720

tcagcggtag ccgcccacca tctcaggtgt ctcgatctgg gggagtttcc tgttttcaga    780

ttacttctct cttcttgtcg gggaagctgc ccctccgtcc catcctttcc cagggccttc    840

cgggggcggc tcggtgggcc tccagtccgg ctctctggcc acgggaggcc ctcatcagcc    900

tgccggtcaa cctgagggac gaagtgtgtt gtccggcacc cctggagagg cccaaa        956
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<210> 272
<211> 231
<212> PRT
<213> Homo sapiens

<400> 272

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Ala Ala Leu Tyr Gly Ala Ser Gly His Phe Ala Pro Gly Thr Thr Val
1               5                   10                  15

Pro Leu Ala Leu Pro Pro Gly Gly Asn Gly Ser Ala Thr Pro Asp Asn
            20                  25                  30

Gly Thr Thr Pro Gly Ala Glu Gly Trp Arg Gln Leu Leu Gly Leu Leu
        35                  40                  45
```

```
Pro Glu His Met Ala Glu Lys Leu Cys Glu Ala Trp Ala Phe Gly Gln
    50                  55                  60

Ser His Gln Thr Gly Val Val Ala Leu Gly Leu Leu Thr Cys Leu Leu
65                  70                  75                  80

Ala Met Leu Leu Ala Gly Arg Ile Arg Leu Arg Arg Ile Asp Ala Phe
                85                  90                  95

Cys Thr Cys Leu Trp Ala Leu Leu Leu Gly Leu His Leu Ala Glu Gln
            100                 105                 110

His Leu Gln Ala Ala Ser Pro Ser Trp Leu Asp Thr Leu Lys Phe Ser
        115                 120                 125

Thr Thr Ser Leu Cys Cys Leu Val Gly Phe Thr Ala Ala Val Ala Thr
    130                 135                 140

Arg Lys Ala Thr Gly Pro Arg Arg Phe Arg Pro Arg Arg Phe Phe Pro
145                 150                 155                 160

Gly Asp Ser Ala Gly Leu Phe Pro Thr Ser Pro Ser Leu Ala Ile Pro
                165                 170                 175

His Pro Ser Val Gly Gly Ser Pro Ala Ser Leu Phe Ile Pro Ser Pro
            180                 185                 190

Pro Ser Phe Leu Pro Leu Ala Asn Gln Ala Ala Leu Pro Val Ser Ser
        195                 200                 205

Thr Asp Leu Thr Leu Leu Ile Cys Leu Ala Ala Ser Ala Gly Pro Ser
    210                 215                 220

Leu Trp Glu Pro Tyr Pro Leu
225                 230
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<210> 273
<211> 1806
<212> DNA
<213> Homo sapiens

<400> 273
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tacccccctg ccggcctgcc gtccttccac gcggagagcc atggagggag tgagcgcgct 180

gctggcccgc tgccccacgg ccggcctggc cggcggcctg ggggtcacgg cgtgcgccgc 240

ggccggcgtg ttgctctacc ggatcgcgcg gaggatgaag ccaacgcaca cgatggtcaa 300

ctgctggttc tgcaaccagg atacgctggt gccctatggg aaccgcaact gctgggactg 360

tccccactgc gagcagtaca acggcttcca ggagaacggc gactacaaca agccgatccc 420

cgcccagtac ttggagcacc tgaaccacgt ggtgagcagc gcgcccagcc tgcgcgaccc 480

ttcgcagccg cagcagtggg tgagcagcca agtcctgctg tgcaagaggt gcaaccacca 540

ccagaccacc aagatcaagc agctggccgc cttcgctccc cgcgaggagg gcaggtatga 600

cgaggaggtc gaggtgtacc ggcatcacct ggagcagatg tacaagctgt gccggccgtg 660

ccaagcggct gtggagtact acatcaagca ccagaaccgc cagctgcgcg ccctgttgct 720

cagccaccag ttcaagcgcc gggaggccga ccagacccac gcacagaact tctcctccgc 780

cgtgaagtcc ccggtccagg tcatcctgct ccgtgccctc gccttcctgg cctgcgcctt 840

cctactgacc accgcgctgt atggggccag cggacacttc gccccaggca ccactgtgcc 900

cctggccctg ccacctggtg gcaatggctc agccacacct gacaatggca ccacccctgg 960

ggccgagggc tggcggcagt tgctgggcct actccccgag cacatggcgg agaagctgtg 1020

tgaggcctgg gcctttgggc agagccacca gacgggcgtc gtggcactgg gcctactcac 1080

ctgcctgctg gcaatgctgc tggctggccg catcaggctc cggaggatcg atgccttctg 1140

cacctgcctg tgggccctgc tgctggggct gcacctggct gagcagcacc tgcaggccgc 1200

ctcgcctagc tggctagaca cgctcaagtt cagcaccaca tctttgtgct gcctggttgg 1260

cttcacggcg gctgtggcca caaggaaggc aacgggccca cggaggttcc ggccccgaag 1320

gttcttccca ggagactctg ccggcctttt ccccaccagc cccagcttgg ccatccctca 1380

cccgagtgtc ggaggctctc cagcgtctct gttcatcccc agcccgccca gcttcctgcc 1440

cctcgccaac caagcagctc ttccggtctc ctcgacggac ctcaccctcc tcatttgcct 1500

ggccgcctca gccgggccct ctctctggga accataccct ctctgactcg agcagactcc 1560

ggctatctgt tcagcggtag ccgcccacca tctcaggtgt ctcgatctgg gggagtttcc 1620

tgttttcaga ttacttctct cttcttgtcg gggaagctgc ccctccgtcc catcctttcc 1680

cagggccttc cgggggcggc tcggtgggcc tccagtccgg ctctctggcc acgggaggcc 1740

ctcatcagcc tgccggtcaa cctgagggac gaagtgtgtt gtccggcacc cctggagagg 1800

cccaaa 1806

<210> 274
<211> 461
<212> PRT
<213> Homo sapiens

<400> 274

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Met Glu Gly Val Ser Ala Leu Leu Ala Arg Cys Pro Thr Ala Gly Leu
1               5                  10                  15

Ala Gly Gly Leu Gly Val Thr Ala Cys Ala Ala Ala Gly Val Leu Leu
            20                  25                  30

Tyr Arg Ile Ala Arg Arg Met Lys Pro Thr His Thr Met Val Asn Cys
        35                  40                  45

Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn Arg Asn Cys
    50                  55                  60

Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln Glu Asn Gly
65                  70                  75                  80

Asp Tyr Asn Lys Pro Ile Pro Ala Gln Tyr Leu Glu His Leu Asn His
                85                  90                  95

Val Val Ser Ser Ala Pro Ser Leu Arg Asp Pro Ser Gln Pro Gln Gln
            100                 105                 110

Trp Val Ser Ser Gln Val Leu Leu Cys Lys Arg Cys Asn His His Gln
        115                 120                 125

Thr Thr Lys Ile Lys Gln Leu Ala Ala Phe Ala Pro Arg Glu Glu Gly
    130                 135                 140

Arg Tyr Asp Glu Glu Val Glu Val Tyr Arg His His Leu Glu Gln Met
145                 150                 155                 160

Tyr Lys Leu Cys Arg Pro Cys Gln Ala Ala Val Glu Tyr Tyr Ile Lys
                165                 170                 175

His Gln Asn Arg Gln Leu Arg Ala Leu Leu Leu Ser His Gln Phe Lys
            180                 185                 190

Arg Arg Glu Ala Asp Gln Thr His Ala Gln Asn Phe Ser Ser Ala Val
        195                 200                 205

Lys Ser Pro Val Gln Val Ile Leu Leu Arg Ala Leu Ala Phe Leu Ala
    210                 215                 220

Cys Ala Phe Leu Leu Thr Thr Ala Leu Tyr Gly Ala Ser Gly His Phe
225                 230                 235                 240

Ala Pro Gly Thr Thr Val Pro Leu Ala Leu Pro Pro Gly Gly Asn Gly
                245                 250                 255
```

```
Ser Ala Thr Pro Asp Asn Gly Thr Thr Pro Gly Ala Glu Gly Trp Arg
            260                 265                 270

Gln Leu Leu Gly Leu Leu Pro Glu His Met Ala Glu Lys Leu Cys Glu
        275                 280                 285

Ala Trp Ala Phe Gly Gln Ser His Gln Thr Gly Val Val Ala Leu Gly
    290                 295                 300

Leu Leu Thr Cys Leu Leu Ala Met Leu Leu Ala Gly Arg Ile Arg Leu
305                 310                 315                 320

Arg Arg Ile Asp Ala Phe Cys Thr Cys Leu Trp Ala Leu Leu Leu Gly
                325                 330                 335

Leu His Leu Ala Glu Gln His Leu Gln Ala Ala Ser Pro Ser Trp Leu
            340                 345                 350

Asp Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu Val Gly Phe
        355                 360                 365

Thr Ala Ala Val Ala Thr Arg Lys Ala Thr Gly Pro Arg Arg Phe Arg
    370                 375                 380

Pro Arg Arg Phe Phe Pro Gly Asp Ser Ala Gly Leu Phe Pro Thr Ser
385                 390                 395                 400

Pro Ser Leu Ala Ile Pro His Pro Ser Val Gly Gly Ser Pro Ala Ser
                405                 410                 415

Leu Phe Ile Pro Ser Pro Pro Ser Phe Leu Pro Leu Ala Asn Gln Ala
            420                 425                 430

Ala Leu Pro Val Ser Ser Thr Asp Leu Thr Leu Leu Ile Cys Leu Ala
        435                 440                 445

Ala Ser Ala Gly Pro Ser Leu Trp Glu Pro Tyr Pro Leu
    450                 455                 460
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<210> 275
<211> 600
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (460)..(460)
<223> n is a, c, g, t or u

<220>
<221> misc_feature
<222> (530)..(530)
<223> n is a, c, g, t or u

<220>
<221> misc_feature
<222> (574)..(574)
<223> n is a, c, g, t or u

<220>
<221> misc_feature
<222> (577)..(577)
<223> n is a, c, g, t or u

<400> 275
tcaagtctga cttgcatcta cactgcgggc aagatgcggc tgcaagaccg catcgccacg 60

ttcttcttcc caaaaggcat gatgctcacc acggctgcgc tgatgctctt cttcttacac 120

ctgggcatct tcatcagaga cgtgcacaac ttctgcatca cctaccacta tgaccacatg 180

agctttcact acacggtcgt cctgatgttc tcccaggtga tcagcatctg ctgggctgcc 240

atggggtcac tctatgctga gatgacagaa aacaagtacg tctgcttctc cgccctgacc 300

atcctgagtg agtggcagga gggggagggt gcaagaggga gcggggagct ttggaaccct 360

gagatgtggc aaggagtagc cagggaaggg tactggggct catgggggggc tctgtccccc 420

gcccagtgct caacggagcc atgctcttca accgcctgtn cttggagttt ctggccatcg 480

agtaccggga ggagcaccac tgaggcctgg ggagtcggaa cagggctaan gaggggggaag 540

caaaaggctg cctcgggtgt tttaataaag ctgntgntta tttccaaaaa aaaaaaaaaa 600

<210> 276
<211> 174
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (128)..(128)
<223> Xaa is S, P, T or A

<220>
<221> UNSURE
<222> (151)..(151)
<223> Xaa is M, T, K or R

<220>
<221> UNSURE
<222> (166)..(166)
<223> Xaa is L, M or V

<220>
<221> UNSURE
<222> (167)..(167)
<223> Xaa is F, L, I or V

<400> 276

Met Met Leu Thr Thr Ala Ala Leu Met Leu Phe Phe Leu His Leu Gly
1 5 10 15

Ile Phe Ile Arg Asp Val His Asn Phe Cys Ile Thr Tyr His Tyr Asp
20 25 30

His Met Ser Phe His Tyr Thr Val Val Leu Met Phe Ser Gln Val Ile
35 40 45

Ser Ile Cys Trp Ala Ala Met Gly Ser Leu Tyr Ala Glu Met Thr Glu
50 55 60

Asn Lys Tyr Val Cys Phe Ser Ala Leu Thr Ile Leu Ser Glu Trp Gln
65 70 75 80

Glu Gly Glu Gly Ala Arg Gly Ser Gly Glu Leu Trp Asn Pro Glu Met
85 90 95

Trp Gln Gly Val Ala Arg Glu Gly Tyr Trp Gly Ser Trp Gly Ala Leu
100 105 110

Ser Pro Ala Gln Cys Ser Thr Glu Pro Cys Ser Ser Thr Ala Cys Xaa
115 120 125

Trp Ser Phe Trp Pro Ser Ser Thr Gly Arg Ser Thr Thr Glu Ala Trp
130 135 140

Gly Val Gly Thr Gly Leu Xaa Arg Gly Lys Gln Lys Ala Ala Ser Gly
145 150 155 160

Val Leu Ile Lys Leu Xaa Xaa Ile Ser Lys Lys Lys Lys Lys
165 170

<210> 277
<211> 457
<212> DNA
<213> Homo sapiens

<400> 277
aaacactgca ggctacgaat cggtcattgc ataggttttc catgaatcag gaagattcag 60

tcctggtaaa ttcattccca ggaacatcgc tgccactgct attattctag cagctgttcc 120

catactccaa tgagtccagt taaacatttg ccttcttggg tcatgtaaag gtggcctgaa 180

gactgccaga agaggctgaa gaactgccaa agtcatcact atacagccga ggtatgggtg 240

gtaacctgca tgcctactcc agcctcccct gtatataaac ggcataacaa aagcaatgca 300

ggtgaggaca gttgtggtga acatgagcat ccgatgcacc tgaaaccaag ctgcttcacc 360

aagcaagaaa gcttttgacc aaactggctt gaagaaccgg gcaaccagta cacctatgct 420

aacagtagtc atccatgcca caaacattaa ggcacca 457

<210> 278
<211> 144
<212> PRT
<213> Homo sapiens

<400> 278

Met Phe Val Ala Trp Met Thr Thr Val Ser Ile Gly Val Leu Val Ala
1 5 10 15

Arg Phe Phe Lys Pro Val Trp Ser Lys Ala Phe Leu Leu Gly Glu Ala
20 25 30

Ala Trp Phe Gln Val His Arg Met Leu Met Phe Thr Thr Thr Val Leu
35 40 45

Thr Cys Ile Ala Phe Val Met Pro Phe Ile Tyr Arg Gly Gly Trp Ser
50 55 60

Arg His Ala Gly Tyr His Pro Tyr Leu Gly Cys Ile Val Met Thr Leu
65 70 75 80

Ala Val Leu Gln Pro Leu Leu Ala Val Phe Arg Pro Pro Leu His Asp
85 90 95

Pro Arg Arg Gln Met Phe Asn Trp Thr His Trp Ser Met Gly Thr Ala
100 105 110

Ala Arg Ile Ile Ala Val Ala Ala Met Phe Leu Gly Met Asn Leu Pro
115 120 125

Gly Leu Asn Leu Pro Asp Ser Trp Lys Thr Tyr Ala Met Thr Asp Ser
130 135 140

<210> 279
<211> 293
<212> DNA
<213> Homo sapiens

<400> 279
ttttttttttt ttttttaag gctgaagcaa ataggaacgt atatttctca tgaatccaaa 60

gcaaagacac aggaagtgct ggcattcttt tggtggctgg tagctcttga ccttctcttc 120

aaggttgcca catgccttag cagcagctca tgacttcacg ttctcaccgt attcgaaggc 180

aggaagcatg gagtagctgg cagctgcgtt tgacacagac tgccctcgga ccccttctcc 240

gcgcagtgcg actcgcaatt gtctggagca cgttggcagc agccctcgtg ccg 293

<210> 280
<211> 45
<212> PRT
<213> Homo sapiens

<400> 280

Arg His Glu Gly Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His
1 5 10 15

Cys Ala Glu Lys Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Leu Pro
20 25 30

Ala Thr Pro Cys Phe Leu Pro Ser Asn Thr Val Arg Thr
35 40 45

<210> 281
<211> 15
<212> PRT
<213> Homo sapiens

<400> 281

Cys Gln Lys Gln Arg Asn Trp His Gly Ile Trp Arg Leu Glu Val
1 5 10 15

<210> 282
<211> 13
<212> PRT
<213> Homo sapiens

<400> 282

Met Ala Lys Gln Gly Glu Met Asn Thr Ser Thr Ser Cys
1 5 10

<210> 283
<211> 13
<212> PRT
<213> Homo sapiens

<400> 283

Pro Lys Arg Gly Gly Arg Ala Gly Arg Glu His Ser Cys
1 5 10

<210> 284
<211> 91
<212> PRT
<213> Homo sapiens

<400> 284

Arg Phe Gln Arg Asn Thr Gly Glu Met Ser Ser Asn Ser Thr Ala Leu
1 5 10 15

Ala Leu Val Arg Pro Ser Ser Ser Gly Leu Ile Asn Ser Asn Thr Asp
20 25 30

Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg Asp Ile Leu Asn Asn Phe
35 40 45

Pro His Ser Ile Ala Arg Gln Lys Arg Ile Leu Val Asn Leu Ser Met
50 55 60

Val Glu Asn Lys Leu Val Glu Leu Glu His Thr Leu Leu Ser Lys Gly
65 70 75 80

Phe Arg Gly Ala Ser Pro His Arg Lys Ser Thr
85 90

<210> 285
<211> 15
<212> PRT
<213> Homo sapiens

<400> 285

Cys Lys Tyr Arg Arg Phe Gln Arg Asn Thr Gly Glu Met Ser Ser
1 5 10 15

<210> 286
<211> 14
<212> PRT
<213> Homo sapiens

<400> 286

Cys Lys Gly Phe Arg Gly Ala Ser Pro His Arg Lys Ser Thr
1 5 10

<210> 287
<211> 19
<212> PRT
<213> Homo sapiens

<400> 287

Met Ala Cys Ile Tyr Pro Thr Thr Phe Tyr Thr Ser Leu Pro Thr Lys
1 5 10 15

Ser Leu Asn

<210> 288
<211> 121
<212> PRT
<213> Homo sapiens

<400> 288

```
Ala Pro Pro Ser Cys Arg Glu Cys Tyr Gln Ser Leu His Tyr Arg Gly
1               5                   10                  15

Glu Met Gln Gln Tyr Phe Thr Tyr His Thr His Ile Glu Arg Ser Cys
            20                  25                  30

Tyr Gly Asn Leu Ile Glu Glu Cys Val Glu Ser Gly Lys Ser Tyr Tyr
        35                  40                  45

Lys Val Lys Asn Leu Gly Val Cys Gly Ser Arg Asn Gly Ala Ile Cys
    50                  55                  60

Pro Arg Gly Lys Gln Trp Leu Cys Phe Thr Lys Ile Gly Gln Trp Gly
65                  70                  75                  80

Val Asn Thr Gln Val Leu Glu Asp Ile Lys Arg Glu Gln Ile Ile Ala
                85                  90                  95

Lys Ala Lys Ala Ser Lys Pro Thr Thr Pro Pro Glu Asn Arg Pro Arg
            100                 105                 110

His Phe His Ser Phe Ile Gln Lys Leu
        115                 120
```

<210> 289
<211> 15
<212> PRT
<213> Homo sapiens

<400> 289

```
Cys Glu Asn Arg Pro Arg His Phe His Ser Phe Ile Gln Lys Leu
1               5                   10                  15
```

<210> 290
<211> 13
<212> PRT
<213> Homo sapiens

<400> 290

```
Cys Ile Tyr Pro Thr Thr Phe Tyr Thr Ser Leu Pro Thr
1               5                   10
```

<210> 291

<211> 14
<212> PRT
<213> Homo sapiens

<400> 291

Cys Lys Glu Asp Glu Leu Val Arg Asp Ser Pro Ala Arg Lys
1 5 10

<210> 292
<211> 12
<212> PRT
<213> Homo sapiens

<400> 292

Ala Leu Gly Thr Arg Leu Ser Gln His Thr Asp Val
1 5 10

<210> 293
<211> 11
<212> PRT
<213> Homo sapiens

<400> 293

Asp Phe Asn Cys Pro Cys Leu Val His Tyr Asn
1 5 10

<210> 294
<211> 53
<212> PRT
<213> Homo sapiens

<400> 294

Ser Ser Ser Val Asp Pro Glu Lys Phe Leu Asp Phe Ala Asn Met Thr
1 5 10 15

Pro Ser Gln Val Gln Leu Phe Leu Ala Lys Val Pro Cys Lys Glu Asp
20 25 30

Glu Leu Val Arg Asp Ser Pro Ala Arg Lys Ala Val Ser Arg Tyr Leu
35 40 45

Arg Cys Leu Ser Gln
50

<210> 295
<211> 146
<212> PRT
<213> Homo sapiens

<400> 295

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Arg Cys Leu Arg Pro Cys Phe Asp Gln Thr Val Phe Leu Gln Arg Arg
1               5                   10                  15

Tyr Trp Ser Asn Tyr Val Asp Leu Glu Gln Lys Leu Phe Asp Glu Thr
            20                  25                  30

Cys Cys Glu His Ala Arg Asp Phe Ala His Arg Cys Val Leu His Phe
        35                  40                  45

Phe Ala Ser Met Arg Ser Glu Leu Gln Ala Arg Gly Leu Arg Arg Gly
    50                  55                  60

Asn Ala Gly Arg Arg Leu Glu Leu Pro Ala Val Pro Glu Pro Pro Glu
65                  70                  75                  80

Gly Leu Asp Ser Gly Ser Gly Lys Ala His Leu Arg Ala Ile Ser Ser
                85                  90                  95

Arg Glu Gln Val Asp Arg Leu Leu Ser Thr Trp Tyr Ser Ser Lys Pro
            100                 105                 110

Pro Leu Asp Leu Ala Ala Ser Pro Gly Leu Cys Gly Gly Gly Leu Ser
        115                 120                 125

His Arg Ala Pro Thr Leu Ala Leu Gly Thr Arg Leu Ser Gln His Thr
    130                 135                 140

Asp Val
145
```

<210> 296
<211> 1035
<212> PRT
<213> Homo sapiens

<400> 296

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Met Pro Cys Gly Phe Ser Pro Ser Pro Val Ala His His Leu Val Pro
1               5                   10                  15

Gly Pro Pro Asp Thr Pro Ala Gln Gln Leu Arg Cys Gly Trp Thr Val
            20                  25                  30

Gly Gly Trp Leu Leu Ser Leu Val Arg Gly Leu Leu Pro Cys Leu Pro
        35                  40                  45

Pro Gly Ala Arg Thr Ala Glu Gly Pro Ile Met Val Leu Ala Gly Pro
    50                  55                  60
```

```
Leu Ala Val Ser Leu Leu Leu Pro Ser Leu Thr Leu Leu Val Ser His
65                  70                  75                  80

Leu Ser Ser Ser Gln Asp Val Ser Ser Glu Pro Ser Ser Glu Gln Gln
                85                  90                  95

Leu Cys Ala Leu Ser Lys His Pro Thr Val Ala Phe Glu Asp Leu Gln
            100                 105                 110

Pro Trp Val Ser Asn Phe Thr Tyr Pro Gly Ala Arg Asp Phe Ser Gln
        115                 120                 125

Leu Ala Leu Asp Pro Ser Gly Asn Gln Leu Ile Val Gly Ala Arg Asn
    130                 135                 140

Tyr Leu Phe Arg Leu Ser Leu Ala Asn Val Ser Leu Leu Gln Ala Thr
145                 150                 155                 160

Glu Trp Ala Ser Ser Glu Asp Thr Arg Arg Ser Cys Gln Ser Lys Gly
                165                 170                 175

Lys Thr Glu Glu Glu Cys Gln Asn Tyr Val Arg Val Leu Ile Val Ala
            180                 185                 190

Gly Arg Lys Val Phe Met Cys Gly Thr Asn Ala Phe Ser Pro Met Cys
        195                 200                 205

Thr Ser Arg Gln Val Gly Asn Leu Ser Arg Thr Ile Glu Lys Ile Asn
    210                 215                 220

Gly Val Ala Arg Cys Pro Tyr Asp Pro Arg His Asn Ser Thr Ala Val
225                 230                 235                 240

Ile Ser Ser Gln Gly Glu Leu Tyr Ala Ala Thr Val Ile Asp Phe Ser
                245                 250                 255

Gly Arg Asp Pro Ala Ile Tyr Arg Ser Leu Gly Ser Gly Pro Pro Leu
            260                 265                 270

Arg Thr Ala Gln Tyr Asn Ser Lys Trp Leu Asn Glu Pro Asn Phe Val
        275                 280                 285

Ala Ala Tyr Asp Ile Gly Leu Phe Ala Tyr Phe Phe Leu Arg Glu Asn
    290                 295                 300

Ala Val Glu His Asp Cys Gly Arg Thr Val Tyr Ser Arg Val Ala Arg
305                 310                 315                 320
```

```
Val Cys Lys Asn Asp Val Gly Gly Arg Phe Leu Leu Glu Asp Thr Trp
                325                 330                 335

Thr Thr Phe Met Lys Ala Arg Leu Asn Cys Ser Arg Pro Gly Glu Val
            340                 345                 350

Pro Phe Tyr Tyr Asn Glu Leu Gln Ser Ala Phe His Leu Pro Glu Gln
        355                 360                 365

Asp Leu Ile Tyr Gly Val Phe Thr Thr Asn Val Asn Ser Ile Ala Ala
    370                 375                 380

Ser Ala Val Cys Ala Phe Asn Leu Ser Ala Ile Ser Gln Ala Phe Asn
385                 390                 395                 400

Gly Pro Phe Arg Tyr Gln Glu Asn Pro Arg Ala Ala Trp Leu Pro Ile
                405                 410                 415

Ala Asn Pro Ile Pro Asn Phe Gln Cys Gly Thr Leu Pro Glu Thr Gly
            420                 425                 430

Pro Asn Glu Asn Leu Thr Glu Arg Ser Leu Gln Asp Ala Gln Arg Leu
        435                 440                 445

Phe Leu Met Ser Glu Ala Val Gln Pro Val Thr Pro Glu Pro Cys Val
    450                 455                 460

Thr Gln Asp Ser Val Arg Phe Ser His Leu Val Val Asp Leu Val Gln
465                 470                 475                 480

Ala Lys Asp Thr Leu Tyr His Val Leu Tyr Ile Gly Thr Glu Ser Gly
                485                 490                 495

Thr Ile Leu Lys Ala Leu Ser Thr Ala Ser Arg Ser Leu His Gly Cys
            500                 505                 510

Tyr Leu Glu Glu Leu His Val Leu Pro Pro Gly Arg Arg Glu Pro Leu
        515                 520                 525

Arg Ser Leu Arg Ile Leu His Ser Ala Arg Ala Leu Phe Val Gly Leu
    530                 535                 540

Arg Asp Gly Val Leu Arg Val Pro Leu Glu Arg Cys Ala Ala Tyr Arg
545                 550                 555                 560

Ser Gln Gly Ala Cys Leu Gly Ala Arg Asp Pro Tyr Cys Gly Trp Asp
```

565 570 575

Gly Lys Gln Gln Arg Cys Ser Thr Leu Glu Asp Ser Ser Asn Met Ser
580 585 590

Leu Trp Thr Gln Asn Ile Thr Ala Cys Pro Val Arg Asn Val Thr Arg
595 600 605

Asp Gly Gly Phe Gly Pro Trp Ser Pro Trp Gln Pro Cys Glu His Leu
610 615 620

Asp Gly Asp Asn Ser Gly Ser Cys Leu Cys Arg Ala Arg Ser Cys Asp
625 630 635 640

Ser Pro Arg Pro Arg Cys Gly Gly Leu Asp Cys Leu Gly Pro Ala Ile
645 650 655

His Ile Ala Asn Cys Ser Arg Asn Gly Ala Trp Thr Pro Trp Ser Ser
660 665 670

Trp Ala Leu Cys Ser Thr Ser Cys Gly Ile Gly Phe Gln Val Arg Gln
675 680 685

Arg Ser Cys Ser Asn Pro Ala Pro Arg His Gly Gly Arg Ile Cys Val
690 695 700

Gly Lys Ser Arg Glu Glu Arg Phe Cys Asn Glu Asn Thr Pro Cys Pro
705 710 715 720

Val Pro Ile Phe Trp Ala Ser Trp Gly Ser Trp Ser Lys Cys Ser Ser
725 730 735

Asn Cys Gly Gly Gly Met Gln Ser Arg Arg Arg Ala Cys Glu Asn Gly
740 745 750

Asn Ser Cys Leu Gly Cys Gly Val Glu Phe Lys Thr Cys Asn Pro Glu
755 760 765

Gly Cys Pro Glu Val Arg Arg Asn Thr Pro Trp Thr Pro Trp Leu Pro
770 775 780

Val Asn Val Thr Gln Gly Gly Ala Arg Gln Glu Gln Arg Phe Arg Phe
785 790 795 800

Thr Cys Arg Ala Pro Leu Ala Asp Pro His Gly Leu Gln Phe Gly Arg
805 810 815

Arg Arg Thr Glu Thr Arg Thr Cys Pro Ala Asp Gly Ser Gly Ser Cys
820 825 830

Asp Thr Asp Ala Leu Val Glu Val Leu Leu Arg Ser Gly Ser Thr Ser
835 840 845

Pro His Thr Val Ser Gly Gly Trp Ala Ala Trp Gly Pro Trp Ser Ser
850 855 860

Cys Ser Arg Asp Cys Glu Leu Gly Phe Arg Val Arg Lys Arg Thr Cys
865 870 875 880

Thr Asn Pro Glu Pro Arg Asn Gly Gly Leu Pro Cys Val Gly Asp Ala
885 890 895

Ala Glu Tyr Gln Asp Cys Asn Pro Gln Ala Cys Pro Val Arg Gly Ala
900 905 910

Trp Ser Cys Trp Thr Ser Trp Ser Pro Cys Ser Ala Ser Cys Gly Gly
915 920 925

Gly His Tyr Gln Arg Thr Arg Ser Cys Thr Ser Pro Ala Pro Ser Pro
930 935 940

Gly Glu Asp Ile Cys Leu Gly Leu His Thr Glu Glu Ala Leu Cys Ala
945 950 955 960

Thr Gln Ala Cys Pro Glu Gly Trp Ser Pro Trp Ser Glu Trp Ser Lys
965 970 975

Cys Thr Asp Asp Gly Ala Gln Ser Arg Ser Arg His Cys Glu Glu Leu
980 985 990

Leu Pro Gly Ser Ser Ala Cys Ala Gly Asn Ser Ser Gln Ser Arg Pro
995 1000 1005

Cys Pro Tyr Ser Glu Ile Pro Val Ile Leu Pro Ala Ser Ser Met
1010 1015 1020

Glu Glu Ala Thr Asp Cys Ala Gly Phe Asn Leu Ile
1025 1030 1035

<210> 297
<211> 16
<212> PRT
<213> Homo sapiens

<400> 297

Cys Pro Tyr Asp Pro Arg His Asn Ser Thr Ala Val Ile Ser Ser Gln
1 5 10 15

<210> 298
<211> 11
<212> PRT
<213> Homo sapiens

<400> 298

Cys Pro Glu Val Arg Arg Asn Thr Pro Trp Thr
1 5 10

<210> 299
<211> 35
<212> PRT
<213> Homo sapiens

<400> 299

Glu Arg Val Trp Ser Asp Asp His Lys Asp Phe Asp Cys Asn Thr Arg
1 5 10 15

Gln Pro Gly Cys Ser Asn Val Cys Phe Asp Glu Phe Phe Pro Val Ser
20 25 30

His Val Arg
35

<210> 300
<211> 38
<212> PRT
<213> Homo sapiens

<400> 300

His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro Val Val Lys Cys His
1 5 10 15

Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe Ile Ser Lys Pro Ser
20 25 30

Glu Lys Asn Ile Phe Thr
35

<210> 301
<211> 15
<212> PRT
<213> Homo sapiens

<400> 301

Cys Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile Leu
1 5 10 15

<210> 302
<211> 13
<212> PRT
<213> Homo sapiens

<400> 302

Glu Arg Val Trp Ser Asp Asp His Lys Asp Phe Asp Cys
1 5 10

<210> 303
<211> 38
<212> PRT
<213> Homo sapiens

<400> 303

Asn Asn Asp Val Ser Cys Asp His Pro Ser Asn Thr Val Pro Ser Gly
1 5 10 15

Ser Asn Gln Asp Leu Gly Ala Gly Ala Gly Glu Asp Ala Arg Ser Asp
20 25 30

Asp Ser Ser Ser Arg Ile
35

<210> 304
<211> 15
<212> PRT
<213> Homo sapiens

<400> 304

Cys Asp His Pro Ser Asn Thr Val Pro Ser Gly Ser Asn Gln Asp
1 5 10 15

<210> 305
<211> 12
<212> PRT
<213> Homo sapiens

<400> 305

Cys Val Pro His Ser Arg Ser Arg Gly Pro Asn Leu
1 5 10

<210> 306
<211> 12
<212> PRT
<213> Homo sapiens

<400> 306

Cys Glu Leu Ser Gln Thr Pro His Pro His Ser Arg
1 5 10

<210> 307
<211> 14
<212> PRT
<213> Homo sapiens

<400> 307

Cys Leu Asp Ser Ala Gly Asn Asn Ala Gly Ile Gln Trp Gly
1 5 10

<210> 308
<211> 14
<212> PRT
<213> Homo sapiens

<400> 308

Cys Asn Arg Val Ser Lys Asn Pro Glu Met Leu Gln Thr Gly
1 5 10

<210> 309
<211> 2115
<212> DNA
<213> Homo sapiens

<400> 309
atgcgtatat gttatgaatg ccaaaatgaa agaacattgt ggcgatgtgt ttcccaggat 60

ggggctgact acagtgtggg cgtgtgtgtc cctgattctt gtgctgaaga ggatgtgact 120

ctgatgtctc ggctggatac tttaagattc agaaatactt cattttggc cccttccctc 180

tttcttttta caataaattc ttcctccttg tctggtggga gtgtgaccag atgtgctgct 240

ggaaagatcc ccctggacac atttgctgcc gtatgtctgt tcatcacctt gctgggtctc 300

atcctccctc cggctggaac agtctgcgtg gcagctaggg aatgggggtc agcctgcagg 360

acatcgcggg aacacgggga acctctggcc acttacggga gtctgccact gagcgaggcg 420

gagagcaatg aacaaagaag cagaatccca cggacacact gccgggcaca tctcctcctg 480

tcagcagcct ccagcagagg aaaaaggttt ctaggagccg tggctcatgc tctggagtgc 540

ttttcttggc agaagaatgt gccagccatc tggactacaa aggcaccagg tggcacctgc 600

tctgcactga atggcattcg tgtcttgagt cttctttgga tcatctcggg acacaccagt 660

cagatgactg catggctgtc tttgggatgg aaagatggag ggcacgaaag gccactggtc 720

atgtctgggc catcagtggg aatcggagac accagagaag ccacgagtgg ttggttaagt 780

gcaagttcgt ttttaaagat gcatcagaat tcagacaaag gaataacccc caaaggcata 840

ctcagatact ttctcagtca cctggtaagg ttgcagcctc ttcacctgta ttcaatgtgc 900

ttgttggttg gactgttctc tcttgttccc tggggacctg tctgggaaat gcccaaattc 960

cactgggata actgccggca agcatggtgg acgaatctgc tgttgctaaa taactttgtg 1020

tcggtcaaga atgcgtgcaa tggctggacc tggtaccttg ccaatgactt ccagttccac 1080

ctcaccacac cagtgattat cttcatccat gtaaagagta cacagatcct catcctcctt 1140

ggggccatgc tgttcttggc atctttcaca gccactgctc tgatcacctt ggcatataaa 1200

cttcctgtcg tggctccatc agaaaccagg acttcccggg gagggctgct gaatgccagg 1260

ctgttcaccc tgtgcccttt ggttcatgga aaaagtgggt atgaaacttt tggtctggat 1320

gggaaagctg attgccttct tgcttccaaa cttctgaacc tttcaacctg cactggaaat 1380

gaacaagtgt gccctaaatg tacctttggg cttgctgatt attccaatgg acatctcagg 1440

gatttggatt ccctttgcca tgtccagatc aaacataaca ttttggctta tttccttgta 1500

tttttcagtg aagaggcgat tgtattgtat ttcgtggagt actacacaaa gccctactgc 1560

cgatttgggc cagttcttgt gggcctcttt ctgagcattt acatgcacca aaaccaccag 1620

gaaaacattc tcagaaccaa gctgcagctc tctaccaagc cctccaccgg accctgtggg 1680

cggcggctgt gggctgagtc ctctttgcgt gccacggagg atatggaggt atggaagcgg 1740

ctccaggctt tgctgtcggg ttcacaccct gttcctttaa aggtgacaaa tcgaacacac 1800

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gacaccaaca tgttctatct tttctctgga caccgtgtgc tgaccttcgt cactgggctg 2040

gccctgacgc tgttcattga gaaaccatgt caggaactga agcagcacct gctgggccat 2100

gaatgttctg gttaa 2115

<210> 310
<211> 704
<212> PRT
<213> Homo sapiens

<400> 310

Met Arg Ile Cys Tyr Glu Cys Gln Asn Glu Arg Thr Leu Trp Arg Cys
1 5 10 15

Val Ser Gln Asp Gly Ala Asp Tyr Ser Val Gly Val Cys Val Pro Asp
20 25 30

Ser Cys Ala Glu Glu Asp Val Thr Leu Met Ser Arg Leu Asp Thr Leu
35 40 45

Arg Phe Arg Asn Thr Ser Phe Leu Ala Pro Ser Leu Phe Leu Phe Thr
50 55 60

```
Ile Asn Ser Ser Ser Leu Ser Gly Gly Ser Val Thr Arg Cys Ala Ala
65                  70                  75                  80

Gly Lys Ile Pro Leu Asp Thr Phe Ala Ala Val Cys Leu Phe Ile Thr
                85                  90                  95

Leu Leu Gly Leu Ile Leu Pro Pro Ala Gly Thr Val Cys Val Ala Ala
            100                 105                 110

Arg Glu Trp Gly Ser Ala Cys Arg Thr Ser Arg Glu His Gly Glu Pro
        115                 120                 125

Leu Ala Thr Tyr Gly Ser Leu Pro Leu Ser Glu Ala Glu Ser Asn Glu
    130                 135                 140

Gln Arg Ser Arg Ile Pro Arg Thr His Cys Arg Ala His Leu Leu Leu
145                 150                 155                 160

Ser Ala Ala Ser Ser Arg Gly Lys Arg Phe Leu Gly Ala Val Ala His
                165                 170                 175

Ala Leu Glu Cys Phe Ser Trp Gln Lys Asn Val Pro Ala Ile Trp Thr
            180                 185                 190

Thr Lys Ala Pro Gly Gly Thr Cys Ser Ala Leu Asn Gly Ile Arg Val
        195                 200                 205

Leu Ser Leu Leu Trp Ile Ile Ser Gly His Thr Ser Gln Met Thr Ala
    210                 215                 220

Trp Leu Ser Leu Gly Trp Lys Asp Gly Gly His Glu Arg Pro Leu Val
225                 230                 235                 240

Met Ser Gly Pro Ser Val Gly Ile Gly Asp Thr Arg Glu Ala Thr Ser
                245                 250                 255

Gly Trp Leu Ser Ala Ser Ser Phe Leu Lys Met His Gln Asn Ser Asp
            260                 265                 270

Lys Gly Ile Thr Pro Lys Gly Ile Leu Arg Tyr Phe Leu Ser His Leu
        275                 280                 285

Val Arg Leu Gln Pro Leu His Leu Tyr Ser Met Cys Leu Leu Val Gly
    290                 295                 300

Leu Phe Ser Leu Val Pro Trp Gly Pro Val Trp Glu Met Pro Lys Phe
305                 310                 315                 320
```

```
His Trp Asp Asn Cys Arg Gln Ala Trp Trp Thr Asn Leu Leu Leu Leu
                325                 330                 335

Asn Asn Phe Val Ser Val Lys Asn Ala Cys Asn Gly Trp Thr Trp Tyr
            340                 345                 350

Leu Ala Asn Asp Phe Gln Phe His Leu Thr Thr Pro Val Ile Ile Phe
        355                 360                 365

Ile His Val Lys Ser Thr Gln Ile Leu Ile Leu Leu Gly Ala Met Leu
    370                 375                 380

Phe Leu Ala Ser Phe Thr Ala Thr Ala Leu Ile Thr Leu Ala Tyr Lys
385                 390                 395                 400

Leu Pro Val Val Ala Pro Ser Glu Thr Arg Thr Ser Arg Gly Gly Leu
                405                 410                 415

Leu Asn Ala Arg Leu Phe Thr Leu Cys Pro Leu Val His Gly Lys Ser
            420                 425                 430

Gly Tyr Glu Thr Phe Gly Leu Asp Gly Lys Ala Asp Cys Leu Leu Ala
        435                 440                 445

Ser Lys Leu Leu Asn Leu Ser Thr Cys Thr Gly Asn Glu Gln Val Cys
    450                 455                 460

Pro Lys Cys Thr Phe Gly Leu Ala Asp Tyr Ser Asn Gly His Leu Arg
465                 470                 475                 480

Asp Leu Asp Ser Leu Cys His Val Gln Ile Lys His Asn Ile Leu Ala
                485                 490                 495

Tyr Phe Leu Val Phe Phe Ser Glu Glu Ala Ile Val Leu Tyr Phe Val
            500                 505                 510

Glu Tyr Tyr Thr Lys Pro Tyr Cys Arg Phe Gly Pro Val Leu Val Gly
        515                 520                 525

Leu Phe Leu Ser Ile Tyr Met His Gln Asn His Gln Glu Asn Ile Leu
    530                 535                 540

Arg Thr Lys Leu Gln Leu Ser Thr Lys Pro Ser Thr Gly Pro Cys Gly
545                 550                 555                 560

Arg Arg Leu Trp Ala Glu Ser Ser Leu Arg Ala Thr Glu Asp Met Glu
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565 570 575

Val Trp Lys Arg Leu Gln Ala Leu Leu Ser Gly Ser His Pro Val Pro
580 585 590

Leu Lys Val Thr Asn Arg Thr His Arg Arg Ala Lys Gln Ile Lys Gly
595 600 605

Phe Asn Gly Lys Glu Ser Ser Pro Gly Leu Val Asn Arg Val Leu Ser
610 615 620

Trp Asp Ile Trp Ser Phe Leu Ser Ser Ile Ser Tyr Ala Arg Tyr Leu
625 630 635 640

Val His Pro Ile Leu Ile Ile Leu Tyr Asn Gly Leu Gln Glu Thr Leu
645 650 655

Ile His His Thr Asp Thr Asn Met Phe Tyr Leu Phe Ser Gly His Arg
660 665 670

Val Leu Thr Phe Val Thr Gly Leu Ala Leu Thr Leu Phe Ile Glu Lys
675 680 685

Pro Cys Gln Glu Leu Lys Gln His Leu Leu Gly His Glu Cys Ser Gly
690 695 700

<210> 311
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 311
aaccgtgtgc tttcttggga c 21

<210> 312
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 312
acattcatgg cccagcagg 19